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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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seq length: 2000000000
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14318.993 Million cell updates/sec
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Listing first 45 summaries
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## ALIGNMENTS

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REFERENCE
AUTHORS
TITLE
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AX085151
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Sequence 1 from Patent W00112798.
AX085151
                                                                                     Loerz,H., Dresselhaus,T., Schreiber,D. and Heuer,S. male sterile plants
Patent: WO 0112798-A 1 22-FFB-2001;
Suedwestdeutsche Saatzucht (DE)
                                                                                                                                                                   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Zea.
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                                            Heuer,S., Loerz,H. and pressure. The MADS box gene ZmMADS2 is specifically und during maize pollen tube growth sex. Plant Reprod. 13, 21-27 (2000)
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Zea mays MADS box protein
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                                                                                                                                Spermatophyta; Magnoliophyta; Liliopsida; clade; Panicoideae; Andropogoneae; Zea.
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                           Heuer, S., Dresselhaus, T. and Loerz, H.
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 (09-DEC-1998) Centre for Applied Molecular Plant Biology,
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                                                                     agttatagatcggtacggcaaggccaaggaagagcagcaagtcgtcgcaaatcccaactc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /translation="MGRGKIVIRRIDNSTSRQVTFSKRRNGIFKKAKELAILCDAEVG LVIFSSTGRLYEE'SSTSMKSVIDRYGKAKEEQQVVANPNSELKFWQREAASLRQQLHN LQENYRQLTGDDLSGLNVKELQSLENQLETSLRGVRAKKDHLLIDETHDLNRKASLFH GENTDLYNKINLIRGENDELHKKIYETEGPSGVNRESPTPFNFAVVETRDVPVQLELS TLPQQUNIEPSTAPKLGLQLIP" "TLPQQUNIEPSTAPKLGLQLIP" """
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                                                                                                                                                                                                    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Zea.

1 (bases 1 to 5031)
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Sequence 12 from Patent W00112798.
AX085162
                                                                                                                                                    Suedwestdeutsche Saatzucht
                                                                                                                                                             Patent: WO 0112798-A 12 22-FEB-2001;
                                                                                                                                                                             Male sterile plants
                                                                                                                                                                                      Loerz, H., Dresselhaus, T., Schreiber, D.
                                                                                                                                                                                                                                                  Zea mays
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                    /note="EXON III"
4066. .4166
                                                                                          /organism="Zea mays"
/db_xref="taxon:4577"
1813. .1994
                                          /note="EXON II" 3202. 3258
                                                                   /note="EXON I"
2871. .2954
        /note="EXON
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                                                                                                                          expression in plants Patent: WO 0112799-A 12 22-FEB-2001;
                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 12 from Patent W00112799
                                                                                                          Suedwestdeutsche Saatzucht (DE)
                                                                                                                                                                     Loerz,H., Dresselhaus,T., Schreiber,D. an Regulatory sequences for pollen specific
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/db_xref="taxon:4577"
1813. .1994
                                          /organism="Zea mays"
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4523. .4676
/note="EXON VII"
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4367. .4449
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Pred. No. 1.4e-96;
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                                                                                                                                                                                 GGTCGGCCTCGTCATCTTCTCCAGCACCGGCCGCCTCTACGAGTACTCTAGCACCAG
                                                                                                                                                                                              ggtcggcctcgtcatcttctccagcaccggccgcctctacgagtactctagcaccag
                                                                                                                                                                                                                            CAAGCGCCGGAACGGGATCTTCAAGAAGGCCAAGGAGCTCGCCATCCTCTGCGATGCGGA 1937
                                                                                                                                                                                                                                      caagcgccggaacgggatcttcaagaaggccaaggagctcgccatcctctgcgatgcgga 484
                                                                                                                                                                                                                                                                      GAGGGGAAAGATCGTGATCCGCAGGATCGATAACTCCACGAGCCGGCAGGTGACCTTCTC 1877
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                                                                                                                                                                                                                                                                                                                TGCGCGCGAGCCAGGGTCAAGAAGAG ----AGCTAGCTATAGGCCGGAGATCGATGGG
                                                                                            Y10750
Y10750.1 GI:1816458
                              Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Lamiales; Veronicaceae; Antirrhinum.
                                                                                    DEFH125 protein.
                                                                                                                   A.majus mRNA for DEFH125 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
Zachgo, S. Saedler, H. and Schwarz-Sommer, Z. Saedler, H. and Schwarz-Sommer, Z. MADS-box transcription
                                                               Antirrhinum majus
                                                                         snapdragon.
                                                                                                                             AMDEFH125
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                    (bases 1 to 936)
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4248. .4289
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96.5%;
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Pred. No. 1.4e-96;
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                                                                                                                                                                                                                                                                                                                                        375 TGAAGATCTACACAGATTGGAGAACCAACTAGAGATGAGTTTGCGAGGCGTGCGCATGAA
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attcaactttgcagtagtagaaaccagagatgttcctgtgcaacttgaactcagcacact 1018
                                                                                                                                              TCAAGAGAACAATGAGCTCTATGAGAAGGTAAAACTCCTTCAACAAGAAAACAAGGAATT
                                                                                                                                                                     ccaagaaaatacagacttgtacaataagatcaacctgattcgccaagaaaatgatgagtt 898
                                                                                                                                                                                                                                           AAAGGTACAGATGTTAACCGATGAGGTTCATGAACTTAGGAGAAAGGGACATCTCATCCA
                                                                                                                                                                                                                                                                    gaaggaccatctcttgatagatgagattcacgatttgaatcgaaaggcaagtttatttca
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                                             GTGTAAAAAGGCTTACGGCACAAGGGATGTAAGTGCAGCAAATGGAACTGCCTTGGTTCC
                                                                                acataaaaagatatatgagactgaaggaccaagtggagttaatcggggagtcaccgactcc
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Direct Submission
Submitted (23-JAN-1997) Z.Schwarz-Sommer, MPI fuer
Submitted (23-JAN-1997) Plant Molecular Genetics, Car
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        factor in Antirrhinum with unusual features plant J. 11 (5), 1043-1050 (1997) 97336298
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10, D-50829 Koeln, FRG
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VVIFSSTGKLYEFSSTSMKSIIERHTKTKEDHHQLLNHGSEVKFWQREAATLRQQLQD
LQENHRKLMGEELQGLNVEDLHRLENQLEMSLRGVRMKKVQMLTDEVHELRRKGHLIH
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/protein_id="CAA71739.1"
/db_xref="GI:1816459"
/db_xref="SPTREMBL:P92927"
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/db_xref="taxon:4151"
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                   AGCATGAAGTCGGTTATTGATAGATACAACAAGAGCAAGATCGAGCAACAACAACTATTG 240
                                               agcatgaaatcagttatagatcggtacggcaaggccaaggaagagcagcaagtcgtcgca 599
                                                                                     GCCGAGGTCGGTCTCATCATCTTCTCTAGCACCGGAAAGCTCTATGACTTTGCAAGCTCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (15-JAN-2001) Lab.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 (bases 1 to 687)
Burgeff,C., Liljegren,S.J., Yanofsky,M.F. and Alvarez-Buylla,E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              differentiated tissues of Arabidopsis thaliana
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/db_xref="GI:18478603"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product="MADS-box protein AGL21"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /chromosome="IV"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Arabidopsis thaliana"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (04-MAR-1997) Biology, Ave, Chestnut Hill, MA 02167, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Dunn, K. and Heard, J.
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                                                                                                                  283
                                                                                                                  ω
                                                                                                                                               /product="MADS-box protein"
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ESHRQIMGEELSGLTVKELQGLENQLEISLRGVRMKKEQLFMDEIQELNRKGDIIHQE
NVELYRKVYGTTDKNGTNRVLSLTNGVGIGDDSNRTCESPAQPATETRTTTALMHSLE
                                                                                                              ISVLTCKQGKWTQILISYMNGI"
128 c 179 g 18
                                                                                                                                                                                                                                                                                                                                                                         /note="located in infected cells of alfalfa root nodules;
evolutionarily related to agl 17"
                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Medicago sativa"
/db_xref="taxon:3879"
                                                                                                                                                                                                                                                                                                                   /codon_start=
                                                                                                                                                                                                                                                                                                                                   /function="transcription factor"
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19.9%;
Score 254.8; DB 8
Pred. No. 1.9e-48;
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426 aagcgccggaacgggatcttcaagaaggccaaggagctcgccatcctctgcgatgcggag 485

aggggaaagatcgtgatccgcaggatcgataactccacgagccggcaggtgaccttctcc 425

AGAGGGAAGATCCAGATTAAGAGGATAGAGAACAACAACGAACAGACAAGTAATCTTTTCG 60

Local Similarity

349;

Conservative

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Mismatches 157;

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                                                                                                                                                                                          Direct Submission
Submitted (12-OCT-2000) Biology, University of California
Diego, 9500 Gilman Drive, La Jolla, CA 92093-0116, USA
                                                                                                                                                                                                                                     2 (bases 1 to 916)
Liljegren, S.J. and
                                                                                                                                                                                                                                                                                       Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidop (bases 1 to 916)
Alvarez-Buylla,E.R., Liljegren,S.J., Pelaz,S., Gold,S.E., Burgeff,C., Ditta,G.S., Vergara-Silva,F. and Yanofsky,M.F. MADS-box gene evolution beyond flowers: expression in polendosperm, guard cells, roots and trichomes
                                                                                                                                                                                                                                                                                                                                                                                Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
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                                                                                                                                                                                                                                                 AX085160
Sequence
AX085160
                                                                                                            Eukaryota; Viridiplantae; Streptophyta; Espermatophyta; Magnoliophyta; Liliopsida;
Male sterile plants
Patent: WO 0112798-A 10 22-FEB-2001;
                                                                                     clade; Panicoideae; Andropogoneae;
                                                                                                                                                            Zea mays
                                                                                                                                                                                                                            AX085160.1
                                          Loerz, H., Dresselhaus, T.,
                                                                                                                                                                               Zea mays
                                                               (bases 1 to 310)
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10 from Patent W00112798
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                                            and Heuer,
                                                                                                            Embryophyta; Tracheophyta;
a; Poales; Poaceae; PACC
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agageteecaceagateteeteeteettacettetttggeaegtteggeggegegegeg
                           CTTCGTCTTCCTTCTCCCTTGGGAAACCTGCTGCCTTTGAGCTTTCTTCTTCG
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                                                                                                                                     285;
                                                                                                                                                                                                                                                                                  Patent: WO 0112799-A 10 22-FEB-2001; Suedwestdeutsche Saatzucht (DE)
                                                                                                                                                                                                                                                                                                           Loerz,H., Dresselhaus,T., Schreiber,D. and Heuer,S. Regulatory sequences for pollen specific or pollen expression in plants
                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Viridiplantae; Streptophyta; Embryophy
Spermatophyta; Magnoliophyta; Liliopsida; Poales;
clade; Panicoideae; Andropogoneae; Zea.
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Location/Qualifiers
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112 c 68 g
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95.3%;
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Pred. No. 3.1e-46;
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Science 279 (5349), 407-409
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Department, IACR Rothamsted, Harpenden 2 (bases 1 to 1098)
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HLQECHRKLVGEELSGMNANDLQNLEDQLVTSLKGVRLKKDQLWTNEIRELNRKGQII
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97. .801
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Submitted (23-JAN-1995) Steven D. Rounsley, Biology-0116,
University of California at San Diego, La Jolla, CA 92093-0116, USA
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Diverse roles for MADS box genes in Arabidopsis development
Plant Cell 7 (8), 1259-1269 (1995)
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/function="DNA binding domain"
<1. .619</pre>
                                                                                            /tissue_type="plate grown roots"
/dev_stage="2 weeks old"
                                                                                                                                    /strain="Landsberg erecta"
/db_xref="taxon:3702"
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Ipomoea batatas
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
                                                                                                        Ipomoea batatas MADS-box protein AF396746
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/db_xref="GI:862648"
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LTGVELNGLSVKELQNIESQLEMSLRGIRMKREQILTNEIKELTRKRNLVHHENLELS
RRVQRIHQENVELYKKAYGTSNTNGLGHHELVDQFMNPMHRLGCS"
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                            tgatagatgagattcacgatttgaatcgaa---aggcaagtttatttcaccaagaaaata
                                                                                        ccctggagaatcaattggaaacaagcctgcgtggtgtccgcgcaaagaaggaccatctct
                                                                                                                                                         aaaattatcggcagttgacgggagatgatctttctgggctgaatgtcaaagaactgcagt 732
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TAATTGAACAGATTCAAGAACTAACCCACAAGCAGGGGAGTTTCGTGCACCAGGAAAACT 619
                                                                                                                                                                                                    AACTCAAGTTTTGGCAAATAGAAGTAGCAATTCTGAGGCAACAATTACACAAACATGCAAG
                                                                                                                                                                                                                         agcttaagttttggcaaagggaggcagcaagcttgagacaacaactgcacaacttgcaag
                                                                                                                                                                                                                                                                     TTGAACGCTACAACAAGACACAAGGTGACAGCCTTCAATCCCCTCTGGACCCCAACATTAG
                                                                                                                                                                                                                                                                                               tagatcggtacggcaaggccaaggaaga---gcagcaagtcgtcgcaaatcccaactcgg
                                                                                                                                                                                                                                                                                                                                                            tcatettetecageaceggeegeetetaegagtaetetageaceageatgaaateagtta 555
                                                                   ATCTTGAAAACCAACTGGAAATGAGTTTGAGCGGCATCAGAATGAAGAAGGAACAAATAC
                                                                                                                                         AAGATCATCGGAAAGTAATGGGAGAAG
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                                                                                                                                                                                                                                                                                                                                                                                                        ATGGGTTGTTGAAGAAGGCTATGGAGATGGGGATTCTGTGCGATGCTGAAGTGGGATTGA
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Submitted (02-JUL-2001) Botany, Natio
Submitted (02-JUL-2001) Botany, Natio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Haung, Y.-S.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished
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LMIFSSTGKLHEFATTSIRSVIERYNKTQGDSLQSPLDPTLELKFWQIEVAILRQOLH
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HQENFELFNKFQAYGTSDPNAVNGDTISPYDFTISEESQGHIHFQLPQNFSDLARALY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product="MADS-box protein"
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127. .783
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aiwan 106, Republic of China
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tgcggaggtcggcctcgtcatcttctccagcaccggccgcctctacgagtactcta---g
                                                                                                                        GATGGGGAGGGGAAGATTGAGATTAAGCGGATCGAGAACACCACCAGCCGGCAGGTCAC 192
                                                                                                                                          9atg9g9g9g9gaaagatcgtgatccgcaggatcgataactccacgagccggcaggtgac 418
                                                                                   cttctccaagcgccggaacgggatcttcaagaaggccaaggagctcgccatcctctgcga 478
                                                                                                                                                                                               al Similarity
318; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence update by submitter on May 25, 1999 this sequence version replaced gi:4378067
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (25-MAY-1999) College of Life Sciences,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Li,Q.-Z.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (19-OCT-1998) College of Life Sciences,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Li,Q.-Z., Zhang,X.-S. and Li,X.-G
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Zhang, X.-S., Li,Q.-Z. and Li, X.-G. Regulation of HAG1 expression in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Agricultural University, Daizong, Taian,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission
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Hyacinthaceae; Hyacinthus.
1 (bases 1 to 1061)
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TNLQNTNRTLMGESLSTMSLRELKQLEGRLERGINKIRTKKNELLSAEIEYMQKREAE
                                                                                                                                                                                                                                                                                                                                                                                                       /product="AGAMOUS homolog transcription factor"
/protein_id="AAD19360.2"
/db_xref="GI:4887235"
                                                                                                                                                                                                                                                                                                                                  MHNDNMYLRNKIAENERAQQQMNMLPSTATEYEGIPQFDSRNFLQVSLMEPNNHHYSF
                                                                                                                                                                                                                                                                                                                                                                                       translation="MGRGKIEIKRIENTTSRQVTFCKRRNGLLKKAYELSVLCDAEVA"
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                                                                                                                                                                                                             Pred. No. 2.1e-30;
                                                                                                                                                                                                                                                                                                     250
                                                                                                                                                                                               Mismatches
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                                                                                                                                                                                                                              DB 8;
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271018, P.R.
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271018, P.R.
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Дb Qy В Qy Дb Db Q д Qγ Вb γ Ъ 553 AACAAAAAAGAACGAGCTGTTGTCCGCTGAAATCGAATACATGCAGAAAAGGGAAGCGGA 612 773 cgcaaagaaggaccatctcttgatagatgagattcacgatttgaatcgaaaggcaagttt 832 593 373 253 CGCCGAGGTCGCCCTCATCGTCTTCTCCACCCGCGGCCGCCTCTACGAGTACTCCAACTC 312 TGGGACTGTCTCTGAAGCTAATTCTCAGTATTATCAGCAAGAAGCAACCAAATTACGGCA 432 cgtcgcaaatcccaactcggagcttaagttttggcaaagggaggcagcagcagcttgagaca 652

Search completed: August 11, 2002, 08:37:19 Job time: 10179 sec

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Title:
Perfect score:
Sequence:
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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   SPTREMBL_19:*

1: sp_bacteria.*

2: sp_bacteria.*

3: sp_fungl:*

4: sp_human:*

5: sp_inverteb).

6: sp_mammal:*

7: sp_mhc:*

8: sp_organel.

9: sp_bade:*

10: sp_plant:*

11: sp_rodent:

12: sp_virus:*

13: sp_virus:*

14: sp_unclass

15: sp_bacteri.

17: sp_archeaf

17: sp_archeaf
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Gapop 10.0 , Gapext 0.5
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1216
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
sp_plant:*
sp_virus:*
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sp_vertebrate:*
sp_vertebrate:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

16	15	14	_	12		10	و	œ	7	6	G	4	ω	2	1	Result No. 9
425.5	426.5	427	428.5	431.5	433.5	435	445	544	589	597.5	605	636.5	638.5	729.5	1216	Score
35.0	35.1	35.1	35.2	35.5	35.6	35.8	36.6	44.7	48.4	49.1	49.8	52.3	52.5	60.0	100.0	Query
222	284	225	222	241	238	261	248	218	239	217	240	234	234	234	240	Query Match Length DB
10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	DB
Q9ZTY6	082732	Q9SBK3	Q40766	065111	065112	Q40765	Q41352	Q94ET1	Q9M2M4	Q9FPP0	004061	Q9SI38	049351	P92927	Q9FVN1	ID
Q9zty6 pinus resin		Q9sbk3 cucumis sat				picea ak		•	Q9m2m4 arabidopsis	0	004061 medicago sa	Q9si38 arabidopsis	049351 arabidopsis	P92927 antirrhinum		Description

QΥ

1 MGRGKIVIRRIDNSTSRQVTESKRRNGIFKKAKELAILCDAEVGLVIFSSTGRLYEYSST 60

45	44	43	42	41	40	39	38	37	36	35	34	ω ω	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17
407	408	409	410	412	412	413	414	414	414.5	414.5	415.5	415.5	416	416.5	419.5	419.5	420	420	422	422	422.5	423	•	24.	424.5	424.5	425	425.5
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254	242	244	249	283	244	247	270	258	284	221	264	246	229	254	249	228	262	237	253	252	249	246	228	222	222	222	261	225
10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10
Q9SBK2	Q9ZTV9	082128	Q9MBE2	Q9FE71	Q9XHM3	Q9XGK4	Q9SPN2	Q9SJH3	Q9FE89	Q9LKQ1	Q9ZS30	Q9XFM8	064959	Q9XGJ6	Q9SEV1	Q9ZPK9	064958	Q9SBK1	09хсл8	Q9ST06	Q9SMB3	Q9ZS29	Q40882	Q9ZTW4	Q9ZRC6	Q9S7I9	004406	Q43616
Q9sbk2 cucumis sat	corylus	triticum		physc	·						gerbera	antirrn						cucumis			oryza	Q9zs29 gerbera nyb	, r	4 pinus ra	picea	picea	pinus	petuni

## ALIGNMENTS

<b>3</b> 8 0	DR DR DR DR DR DR DR DR	RC RA	20000g	RESULT O9FVN1 ID OAC ODT ODT ODT ODT
Query Match 100.0%; Score 1216; DB 10; Length 240; Best Local Similarity 100.0%; Pred. No. 1.6e-76; Matches 240; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	EMBL; AR112149; AAG09919.1; HSSP; P11746; 1MNM. InterPro; IPR002487; K-box. InterPro; IPR002100; MADS-box. Pfam; PF01486; K-box; 1. Pfam; PF00319; SRF-TF; 1. PRINTS; PR004104; MADSDOMAIN. SMART; SM00432; MADS; 1. PROSITE; PS00350; MADS_BOX_1; UNKNOWN_1. PROSITE; PS00366; MADS_BOX_2; 1. SBQUENCE 240 AA; 27415 MW; 5D9B41665CDED984 CRC64;	SEQUENCE FROM N.A. STRAIN-A188; Heuer S., Loerz H., Dresselhaus T.; Heuer S., Sex. plant Reprod. 13:21-27(2000).	MADS2.  Zea mays (Maize).  Zea mays (Maize).  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae; PACC clade;  Panicoideae; Andropogoneae; Zea.  NCBI_TaxID=4577;	ULT 1  VN1  OPFVN1  PRELIMINARY; PRT; 240 AA.  OPFVN1.  O1-MAR-2001 (TrEMBLrel. 16, Created) O1-MAR-2001 (TrEMBLrel. 16, Last sequence update) O1-DEC-2001 (TrEMBLrel. 19, Last annotation update) MADS BOX PROTEIN 2.

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P92927

IDP PSEARCH PS
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PROSITE; PS50066; MADS_BOX_2; 1.
SEQUENCE 234 AA; 26882 MW; D699B216D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                factor in Antirrhinum with unusual features.";
Plant J. 11:1043-1050(1997).
EMBL; Y10750; CAA71739.1;
HSSP; P11746; IMNM.
TRANSFAC; T03080; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRINTS; PR00404; MADSDOMAIN. SMART; SM00432; MADS; 1.
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InterPro; IPR002100; MADS-box.
InterPro; IPR001854; Ribosomal_L29.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Antirrhinum majus (Garden snapdragon).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Lamiales; Veronicaceae; Antirrhinum.
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01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF01486; K-box; 1. Pfam; PF00319; SRF-TF; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DEFH125 PROTEIN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=97336298; PubMed=9193074;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Zachgo S., Saedler H., Schwarz-Sommer Z.;
*Pollen-specific expression of DEFH125, a MADS-box transcription
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=4151;
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                                                                                181 CKKAYGTRDVSAANGTALVPFGFAIGREQFEPIQLHLSQ-PEPENIETSRA
                                                                                                                                       181 HKKIYETEGPSGVNRESPTPFNFAVVETRDVPVQLELSTLPQQNNIEPSTA 231
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                                                                                                                                                                                                                                           KELQSLENQLETSLRGVRAKKDHLLIDEIHDLNRKASLFHQENTDLYNKINLIRQENDEL 180
                                                                                                                                                                                                                                                                                                                            SMKSIIERHTKTKEDHHQLLNHGSEVKFWQREAATLRQQLQDLQENHRKLMGEELQGLNV
                                                                                                                                                                                                                                                                                                                                                                                      SMKSVIDRYGKAKEEQQVVANPNSELKFWQREAASLRQQLHNLQENYRQLTGDDLSGLNV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                    EDLHRLENQLEMSLRGVRMKKVQMLTDEVHELRRKGHLIHQENNELYEKVKLLQQENKEL
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Best Local :
                               Q9SI38;
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence up
01-DEC-2001 (TrEMBLrel. 19, Last annotation
Arabidopsis thaliana (Mouse-ear
              PUTATIVE MADS-BOX PROTEIN ANR1. AT2G14210.
                                                                                                  098138
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01-JUN-1998
01-DEC-2001
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PROSITE; PS50066; MADS_BOX_2;
DNA-binding; Nuclear protein;
SEQUENCE 234 AA; 26805 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Zhang H., Forde B.G.;
"An Arabidopsis MADS box gene that controls nutrient-induced changes in root architecture.";
Science 279:407-409(1998).
-!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
-!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
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InterPro; IPR002100; MADS-box.
Pfam; PF01486; K-box; 1
Pfam; PF00319; SRF-TE; 1
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STRAIN=LANDSBERG ERECTA (LER)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ANR1 , MADS-BOX PROTEIN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Arabidopsis thaliana (Mouse-ear cress).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        049351
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                                                                                                                                                                                                                                                                                                                                                                                                                1 MGRGKIVIRRIDNSTSRQVTFSKRRNGIFKKAKELAILCDAEVGLVIFSSTGRLYEY-SS 59
                                                                                                                                                                       RLGLQL
                                                                                                                                                                                                                                                     LHKKIY----ETEGPSGVNRESPTPFNFAVVETRDVPVQLELSTL---PQQNNIEPSTAP
                                                                                                                                                                                                                                                                                                                                                                   TSMKSVIDRYGKAKEEQQVVANPNSELKFWQREAASLRQQLHNLQENYRQLTGDDLSGLN 119
                                                                                                                                                                                                                             LQKKVHGRTNVIEGNSSVDPISNGTTTYA-----PPQLQLIQLQPAPREKSI-----
                                                                                                                                                                                                                                                                                                              VKELQSLENQLETSLRGVRAKKDHLLIDEIHDLNRKASLFHQENTDLYNKINLIRQENDE 179
                                                                                                                                                                                                                                                                                                                                           SSMKTIIERYNRVKEEQHQLLNHASEIKFWQREVASLQQQLQHLQECHRKLVGEELSGMN 120
                                                                                                                                                                                                                                                                                                                                                                                                 MGRGKIVIRRIDNSTSRQVTFSKRRSGLLKKAKELSILCDAEVGVIIFSSTGKLYDYASN 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Z97057; CAB09793.1;
P11831; 1SRS.
                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (TrEMBLrel. 06, Created)
(TrEMBLrel. 06, Last sequence update)
(TrEMBLrel. 19, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          52.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       47; Mismatches
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2; 1.
.n; Transcription regulation.
MW; 721A03A018E25527 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 638.5;
Pred. No. 1e
                                                       sequence update)
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RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRINTS; PR00404; MADSDOMAIN.
SMART; SM00432; MADS; 1.
PROSITE; PS00350; MADS_BOX_1; 1.
PROSITE; PS50066; MADS_BOX_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
--- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
--- SIMILARITY: TO THE MADS DOMAIN FAMILY OF TRANSCRIPTION FACTORS EMBL; AC007210; AAD25638.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lin
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                         01-JUL-1997 (TrembLrel. 04, 01-JUL-1997 (TrembLrel. 04, 01-DEC-2001 (TrembLrel. 19, MADS-BOX PROTEIN (FRAGMENT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00319; SRF-TF; 1
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InterPro; IPR002100; MADS-box.
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                                                                                                                                                       004061;
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Medicago sativa (Alfalfa)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SSMKTIIERYNRVKEEQHQLLNHASEIKFWQREVASLQQQLQYLQECHRKLVGEELSGMN
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                                                                                                                                                                                                                                                                                                                                        RLGLQL 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                               LQKKVHGRTNAIEGNSSVDPISNGTTTYA-----PPQLQLIQLQPAPREKSI-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LHKKIY----ETEGPSGVNRESPTPFNFAVVETRDVPVQLELSTL---PQQNNIEPSTAP
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                                                                                                                                                                                       PRELIMINARY;
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                                                             Last annotation update
                                                                                                                          Created)
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Pred. No. 1.4e-36;
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Q9FPP0;
01-MAR-2001
01-MAR-2001
01-DEC-2001
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SEQUENCE
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                                                                                                "MADS-box gene evolution beyond flowers: expression endosperm, guard cells, roots and trichomes."; Plant J. 24:457-466(2000).

EMBL; AF312662; AA37899 1; .
InterPro; IPR002487; K-box.
InterPro; IPR002100; MADS-box.
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                      Pfam; PF01486; K-box; 1. Pfam; PF00319; SRF-TF; 1 SMART; SM00432; MADS; 1.
                                                                                                                                                                                                                                                              TISSUE-LEAF, STEM, ROOT;
MEDLINE-20566573; PubMed-11115127;
Alvarez-Buylla E.R., Liljegren S.J., Pelaz S., Gold S.E.,
Ditta G.S., Vergara-Silva F., Yanofsky M.F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosideurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAR-2001 (TrEMBLrel. 16, Last sequence update) 01-DEC-2001 (TrEMBLrel. 19, Last annotation update) MADS-BOX PROTEIN AGL16 (FRAGMENT).
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                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=3702;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KIYETEGPSGVNR---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LQGLENQLEISLRGVRMKKEQLEMDEIQELNRKGDIIHQENVELY--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RSVIGRYNKSKEEHNQLGSTASEIKFGQREAAVLRQQLHNLQESHRQIMGEELSGLTVKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KSVIDRYGKAKEEQQVVANPNSELKFWQREAASLRQQLHNLQENYRQLTGDDLSGLNVKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RGKIQIKRIENTTNRQVIFSKRRNGLLKKAKELAILCDAEVGVMIFSSTAKLYDFASTSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
PS50066; MADS_BOX_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    T03108;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    240 AA; 27138 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fabales; Fabaceae; Papilionoideae; Trifolieae; Medicago
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (TrEMBLrel. 16,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        49.8%;
53.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 32; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            B
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Best Local
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01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
MADS-BOX TRANSCRIPTION FACTOR-LIKE PROTEIN.
                                                                                                                                                                        PROSITE; PS00350; MADS_BOX_1; UNKNOWN_1.
PROSITE; PS50066; MADS_BOX_2; 1.
SEQUENCE 239 AA; 27233 MW; CE420AC4F
                                                                                                                                                                                                               PRINTS; PR00404; MADSDOMAIN. SMART; SM00432; MADS; 1.
                                                                                                                                                                                                                                                                                    EU Arabidopsis sequencing project;
Submitted (JAN-2000) to the EMBL/G
EMBL; AL137080; CAB68129.1; -.
HSSP; P11746; 1MNM.
                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Viridiplantae; Streptophyta; Embry
Spermatophyta; Magnoliophyta; eudicotyledons;
eurosids II; Brassicales; Brassicaceae; Arabi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NON_TER
SEQUENCE
                                                                                                                                                                                                                                                            InterPro; IPR002487; K-box.
InterPro; IPR002100; MADS-box.
                                                                                                                                                                                                                                                                                                                                                           Submitted (JAN-2000)
                                                                                                                                                                                                                                                                                                                                                                      Benes V., Rechmann S.,
Mayer K.F.X., Quetier
                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Arabidopsis thaliana (Mouse-ear cress).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q9M2M4
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                                                                             MGRGKIVIRRIDNSTSRQVTFSKRRNGIFKKAKELAILCDAEVGLVIFSSTGRLYEYSST 60
                    SMKSVIERYSDAKGETSSENDPASEI - - -
                                        SMKSVIDRYGKAKEEQQVVANPNSELKFWQREAASLRQQLHNLQ-ENY------RQL 110
                                                                 {\tt MGRGKIAIKRINNSTSRQVTFSKRRNGLLKKAKELAILCDAEVGVIIFSSTGRLYDFSSS}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DMRDTSNEHVHLQLSQ-PQHDHETHSKAIQL 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AVVETRDVPVQLELSTLPQQNNIEPSTAPKL 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LLIDEIHDLNRKASLFHQENTDLYNKINLIRQENDELHKKIYETEGPSGVNRESPTPFNF
                                                                                                                                                                                                                                  PF01486; K-box; 1.
PF00319; SRF-TF; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEIQFWQKEAAILKRQLHNLQENHRQMMGEELSGLSVEALQNLENQLELSLRGVRMKKDQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RRNGLLKKAKELAILCDAEVGVIIFSSTGRLYDFSSSSMKSVIERYSDAKGETSSENDPA
                                                                                                                    130;
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122; Conserv
                                                                                                                               Similarity
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                                                                                                                  Conservative
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N-2000) to the
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F., Salanoubat M.;
o the EMBL/GenBank/DDBJ d
                                                                                                                  39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         38;
                                                                                                                                                                                                                                                                                                          EMBL/GenBank/DDBJ databases
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Pred. No. 6.1e-34;
"" omatches 50;
                                                                                                                             Pred.
                                                                                                                                         Score
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                                                                                                                                                                         CE420AC4F98D45DB CRC64;
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                                                                                                                                       589;
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                                                                                                                                         DB 10;
                 -QEMYIVTLEKYAYSEELVLDRQM
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                            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllidae; Caryophyllales; Caryophyllaceae; Silene.
                                                                                                                                                                                  Q41352
Q41352;
                                                               SLM1 PROTEIN.
SLM1.
Silene latifolia.
Eukaryota; Viridiplantae;
                                                                                                                            01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
NCBI_TaxID=37657; [1]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (JUL-2001) to the EMBL/GenBank/DDBJ EMBL; AF396746; AAK83920.1; -. SEQUENCE 218 AA; 25222 MW; 788D47FEE8D02DX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Haung Y.-S., Yeh K.-W.;
"Cloning and characterization of a full-length cDNA encoding box protein from sweet potato.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Convolvulaceae; Ipomoea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MADS-BOX PROTEIN.
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                                                                                                                                                                                                                                                                                                                 ELHKKIYETEGPSGVNRESPTPFNFAVVETRDVPVQLELSTLPQ 222
                                                                                                                                                                                                                                                                                                                                                                                  VKELQSLENQLETSLRGVRAKKDHLLIDEIHDLNRK-ASLFHQENTDLYNKINLIRQEND
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                                                                                                                                                                                                                                                                                                                                                    VKDLQNLENQLEMSLSGIRMKKEQILIEQIQELTHKQGSFVHQENFELFNKF--
                                                                                                                                                                                                                                                                                                                                                                                                                     SIRSVIERYNKTQGDSLQSPLDPTLELKFWQIEVAILRQQLHNMQEDHRKVMG-EVYGLS 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                 SMKSVIDRYGKAK-EEQQVVANPNSELKFWQREAASLRQQLHNLQENYRQLTGDDLSGLN 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APKL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        112;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 544;
Pred. No. 3
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Best Local
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InterPro; IPR002100; MADS-box.
Pfam; PF01486; K-box; 1.
Pfam; PF00319; SRF-TF; 1.
PRINTS; PR00404; MADSDOMAIN.
SMART; SM00432; MADS; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; X80488; CAA56655.1; -. HSSP; P11746; 1MNM. TRANSFAC; T03173; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Comparison of MADS-box gene expression in developing "Comparison of the dioectous plant white campion."; plant Cell 6:1775-1787(1994).
                                                                                                                                                                                                                                                                                                         Q40765; PRELIMINARY;
Q40765; O1-NOV-1996 (TrEMBLrel. 01,
01-NOV-1996 (TrEMBLrel. 01,
01-DEC-2001 (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. MEDLINE=95170282; PubMed=7866023;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS00350; MADS_BOX_1; 1.
PROSITE; PS50066; MADS_BOX_2; 1.
DNA-binding; Nuclear protein; Transcription regulation.
SEQUENCE 248 AA; 28347 MW; 20F094B0EA7B3F16 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
                            TRANSFAC; T03075; -.
InterPro; IPR002487; K-box.
InterPro; IPR002100; MADS-box.
                                                                                                                                                    MEDLINE-95170009; PubMed=7865797;
Tandre K., Albert V.A., Sundas A., Engstrom P.;
"Conifer homologues to genes that control floral development
                                                                                                                                                                                                                                       Picea abies (Norway spruce) (Picea excelsa).
Eukaryota; Viridiplantae; Streptophyta; Embr
Spermatophyta; Coniferopsida; Coniferales; P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE;
                                                                                                                                         angiosperms.";
                                                                                                                                                                                                  SEQUENCE FROM N.A.
                 Pfam;
                                                                                                                             Plant Mol.
                                                                                                  -! - SIMILARITY: TO THE MADS DOMAIN
                                                                                                                 -!- SUBCELLULAR LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                          196
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                                                                                                                                                                                                                                                                                                                                                                                                                                        AQQSMSLMPGGSSEYELAPPPQSF-----DSRNYFQVNAL-QPNNTHYSRPDQTTLQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LHKKIYETEGPSGVNRESPTPFNFAVVETRDVPVQLELSTLPQQNNIEPSTAPKLGLQL 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VKELQSLENQLETSLRGVRAKKDHLLIDEIHDLNRKASLFHQENTDLYNKINLIRQENDE 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MKDLKSLENKLERGISRIRSKKNELLFAEIEFMQKREVELHNNNQYLRAKI----AENER 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SVKGTIDRYKKASSDNSGASSAAEANAQYYQQEAAKLRNQIRTVTENNRHLMGEGLSSLN 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SMKSVIDRYGKAKEEQQVVAN-PNSELKFWQREAASLRQQLHNLQENYRQLTGDDLSGLN 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LGRGKIEIKRIENTINRQVTFCKRRNGLLKKAYELSVLCDAEVALIVFSSRGRLYEYANH 79
                                                                      X80902; CAA56864.1;
P11831; 1SRS.
    PF00319;
                 PF01486;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                             Biol. 27:69-78(1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                K-box; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                36.6%;
                                                                                                                 NUCLEAR (BY SIMILARITY)
                                                                                                                                                                                                                                                         Streptophyta; Embryophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    44;
                                                                                                                                                                                                                                                                                                              Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                                                                                                                          Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 445; DB 10,
Pred. No. 2.3e-23,
4; Mismatches 8:
                                                                                                                                                                                                                                          Coniferales; Pinaceae;
                                                                                                    FAMILY
                                                                                                                                                                                                                                                                                                                                                                       261
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                                                                                                                                                                                                                                                                                                              update)
                                                                                                     TRANSCRIPTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 248;
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                                                                                                                                                                                                                                                         Tracheophyta;
                                                                                                                                                                                                                                             Picea.
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RESULT
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Best Local Similarity
Matches
           Query Match
Best Local :
                                                                                                                       InterPro; IPR002487; K-box.
InterPro; IPR002100; MADS-box.
Pfam; PF01486; K-box; 1.
Pfam; PF00319; SRF-TF; 1.
PRINTS; PR00404; MADSDOMAIN.
SMART; SM00432; MADS; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                      065112;
01-AUG-1998
01-AUG-1998
01-DEC-2001
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PROSITE: PS50066; MADS_BOX_2;
DNA-binding; Nuclear protein;
SEQUENCE 261 AA; 29995 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRINTS; PR00404; MADSDOMAIN. SMART; SM00432; MADS; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           065112
                                                                PROSITE; PS00350; WADS_BOX_1; 1.

PROSITE; PS50066; MADS_BOX_2; 1.

DNA-binding; Nuclear protein; Transcription regulation SEQUENCE 238 AA; 27274 MW; C5C3A34454694A2A CRC64;
                                                                                                                                                                                                        -!- SIMILARITY: TO THE MADS DOMAIN FAMILY OF TRANSCRIPTION EMBL; AF052571; AAC06238.1; -. HSSP; P11746; IMNM.
                                                                                                                                                                                                                                                               Brunner A.M., Rottmann W.H., Sheppard L.A., Strauss S.H. "Two Populus trichocarpa genes homologous to AGAMOUS."; Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                               Spermatophyta; Magnoliophyta; eudicotyledons; eurosids I; Malpighiales; Salicaceae; Populus
                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Viridiplantae; Streptophyta;
                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=3694;
                                                                                                                                                                                                                                                                                                                                                                                           Populus trichocarpa (Western balsam poplar)
                                                                                                                                                                                                                                                                                                                                                                                                          PTAG2
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                                                                                                                                                                                                                                                  SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LQKKLSETEGRDVITGIEQTSNTNTGTNGPWDSSITNT----AYALSH-PQQNSNASLH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SMKSVIDRYGKAK-EEQQVVANPNSELKFWQREAASLRQQLHNLQENYRQLTGDDLSGLN
98;
              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                      (TrEMBLrel. 07, Created)
(TrEMBLrel. 07, Last sequence update)
(TrEMBLrel. 19, Last annotation update)
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Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
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38.8%;
             35.6%;
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  39;
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Pred. No. 1
Score 433.5;
Pred. No. 1.4e
99; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
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              1.4e-22;
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.2e-22;
                                                                                                                                                                                                                                                                                                                                                                                 Embryophyta; Tracheophyta;
                            DB 10;
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  54;
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  Indels
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  19;
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1 MGRGKIVIRRIDNSTSRQVTFSKRRNGIFKKAKELAILCDAEVGLVIFSSTGRLYEYSST 60

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RESULT
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ID 06
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PS00350; MADS_BOX_1; 1.

PROSITE; PS50066; MADS_BOX_2; 1.

DNA-binding; Nuclear protein; Transcription regulation.

SEQUENCE 241 AA; 27559 MW; 4C2BFD11F29E99CF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRINTS; PR00404; MADSDOMAIN. SMART; SM00432; MADS; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosid eurosids 1; Malpighiales; Salicaceae; Populus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-AUG-1998 (TrEMBLrel. 07, Created)
01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF01486; K-box; 1. Pfam; PF00319; SRF-TF; 1.
                                230
                                                                          187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR002487; K-box.
InterPro; IPR002100; MADS-box.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
-!- SIMILARITY: TO THE MADS DOMAIN FAMILY OF TRANSCRIPTION FACTORS.
EMBL. AP052570; AAC06237.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=3694;
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                                                                                                                                                                                                                                             76
                                                                                                                                                                                                                                                                                                                     16 LGRGKVEIKRIENTTNRQVTFCKRRSGLLKKAYELSVLCDAEVALIVFSSRGRLYEYSND 75
                                                                                                                                                                                                                                                                                                                                                                                                                                  Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    187 AENE--RKRQHMNLMPGGVNFEIMQSQPFD 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         134
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                                                                                                                                                                                                                                                                                                                                                  1 MGRGKIVIRRIDNSTSRQVTFSKRRNGIFKKAKELAILCDAEVGLVIFSSTGRLYEYSST
                                                                                                                                                                                                                                                                            SMKSVIDRYGKAKEEQQ----VVANPNSELKFWQREAASLRQQLHNLQENYRQLTGDDLSG 117
                              TAPKLGLQLI 239
                                                                          SENERK - -
                                                                                                          DELHKKIYETEGPSGVNRES----PTPFNFAVVETRDVPVQLELSTLPQQNNIEP----S
                                                                                                                                                                                  LNVKELQSLENQLETSLRGVRAKKDHLLIDEIHDLNRKASLFHQENTDLYNKINLIRQEN 177
                                                                                                                                                                                                                                  SVKSTIERYKKASADSSNTGSVSEANAQ--YYQQEAAKLRSQIGNLQNSNRHMLGEALSS
                                                                                                                                               LSVKELKSLEIRLEKGISRIRSKKNELLFAEIEYMQKR-----EVDLHNNNQLLRAKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LNVKELQSLENQLETSLRGVRAKKDHLLIDEIHDLNRKASLFHQENTDLYNKINLIR---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LSYKELKSLEIKLEKGIGRIRSKKNELLFAEIEYMQKR-----EIDLHNNNQLLRAKI
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                35.5%;
40.0%;
                                                                   -RQSMNLMPGGADFEIVQSQ----PYDSRNYSQVNGLQPASHYS
                                                                                                                                                                                                                                                                                                                                                                                                             52; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 431.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No. 1
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                                                                                                                                                                                                                                                                                                                                                                                                             63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      core eudicots; Rosidae;
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    Q9SBK3
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Best Local
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InterPro; IPR002100; MADS-box.
Pfam; PF01486; K-box; 1.
Pfam; PF00319; SRF-TF; 1.
PRINTS; PR00404; MADSDOMAIN.
SMART; SM00432; MADS; 1.
                                                                                                                                                                                                                                                      Q9SBK3
eurosids I; Cucu
NCBI_TaxID=3659;
[1]
                                                                                                                            CAG1.
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01-NOV-1996
01-DEC-2001
                                                                                                                                               AGAMOUS-LIKE PUTATIVE TRANSCRIPTION
                                                                                                                                                                                                          Q9SBK3;
01-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=95170009; PubMed=7865797;
Tandre K., Albert V.A., Sundas A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TRANSFAC; T03076;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Plant Mol. Biol. 27:69-78(1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        angiosperms."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                      PRELIMINARY;
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01,
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01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Cucumis sativus (Cucumber).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosid eurosids I; Cucurbitales; Cucurbitaceae; Cucumis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS00350; MADS_BOX_1; 1.
PROSITE; PS50066; MADS_BOX_2; 1.
PROSITE; PS50066; MADS_BOX_2; 1.
PROSITE; PS50066; MADS_BOX_2; 1.
PROSITE; PS50066; MADS_BOX_2; 1.
PROSITE; PS50066; MADS_BOX_1; 1.
PROSITE; PS00350; MADS_BOX_2; 1.
PROSITE; PS50066; 
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta;
Spermatophyta; Coniferopsida; Coniferales; Pinaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 118 LNYKELQSLENQLETSLRGVRAKKDHLLIDEIHDLNRKASLFHQENTDLYNKI 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MGRGKIVIRRIDNSTSRQVTFSKRRNGIFKKAKELAILCDAEVGLVIFSSTGRLYEYSST
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Last annotation update)
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Best Local
EU Arabidopsis sequencing project;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
-!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
-!- SIMILARITY: TO THE MADS DOMAIN FAMILY OF TRANSCRIPT!
                                                                                                                                                                                                  01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
FLORAL HOMEOTIC PROTEIN AGAMOUS.
MADS OR F13C5.130 OR AT4G18960.
Arabidopsis thallana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosida
                                                                                                                                                                                                                                                                                                                     082732
082732;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
Bevan M., Pohl T., Weizenegger T., Bancroft I., Mewes H.W., Mayer
                                                                             Pohl T., Weizenegger T., Mev
Submitted (MAR-2000) to the
                                                                                                                            Submitted (FEB-1998) to the EMBL/GenBank/DDBJ databases
                                                                                                                                             Schueller
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRINTS; PR00404; MADSDOMAIN.
SMART; SM00432; MADS; 1.
PROSITE; PS00350; MADS_BOX_1;
PROSITE; PS50066; MADS_BOX_2;
                                                       SEQUENCE FROM N.A.
                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                            NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS00350; MADS_BOX_1; 1.
PROSITE; PS50066; MADS_BOX_2; 1.
DNA-binding; Nuclear protein; Transcription regulation.
SEQUENCE 225 AA; 25874 MW; DF5DA59ECE9EC24F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR002487; K-box.
InterPro; IPR002100; MADS-box.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=98399593; PubMed=9729894;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. TISSUE=FLOWER;
                                                                                                                                                                                                                                                                                                                                                                                                 181 N 181
                                                                                                                                                                                                                                                                                                                                                                                                                         177
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            VKELQSLENQLETSLRGVRAKKDHLLIDEIHDLNRKASLFHQENTDLYNKI---NLIRQE 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIKTTIERYKKACSDSSATSSVTELNTQYYQQESAKLRQQIQMLQNSNRHLMGDSLSALT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SMKSVIDRYGKAKEEQQVVANPNS-ELKFWQREAASLRQQLHNLQENYRQLTGDDLSGLN 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PF00319; SRF-TF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  l Similarity
88; Conserv
                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          35.1%;
48.6%;
                                                                                         T., Mewes H.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  35;
                                                                             wes H.W., Lemcke K., Mayer K
EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 427; DB 10;
Pred. No. 3.6e-22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                  8
     TRANSCRIPTION FACTORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 54;
                                                                                          Mayer K.F.X.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
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                                                                                                                                                                                                                   Rosidae;
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                                                                                                                                                                                                                                                                                                                     Best Local
                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF01486; K-box; 1.
Pfam; PF00319; SRF-TF; 1.
PRINTS; PR00404; MADSDOMAIN.
SMART; SM00432; MADS; 1.
                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS00350; MADS_BOX_1; 1.
PROSITE; PS50066; MADS_BOX_2; 1.
DNA-binding; Nuclear protein; Transcription regulation DNA-binding; Nuclear protein; 12BCD6FFCD846DDB CRC64; SEQUENCE 284 AA; 32464 MW; 12BCD6FFCD846DDB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR002487; K-box.
InterPro; IPR002100; MADS-box
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AL021711; CAA16753.1;
EMBL; AL161549; CAB78898.1;
HSSP; P11746; 1MNM.
                                                                                                                                                119
                                                                                        179
                                                                                                                                                                                110
                                                         224
                                                                                                                    168
                                                                                                                                                                                                            62
                                                                                                                                                                                                                                           50
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                                                                                                                                                                            YKGTIERYKKAISDNSNTGSVAEINAQ--YYQQESAKLRQQIISIQNSNRQLMGETIGSM
                                                                                                                                                                                                                                                           GRGKIVIRRIDNSTSRQVTFSKRRNGIFKKAKELAILCDAEVGLVIFSSTGRLYEYSSTS
DOTALOLV
                           PKLGLQLI 239
                                                         RNNPSISLMPGGSNYEQLMPPP-----QTQSQPFDSRNYFQVAAL-QPNNHHYSSAGRQ
                                                                                                                   SPKELRNLEGRLERSITRIRSKKNELLFSEIDYMQKREVDLHNDNQILRAKI----AENE
                                                                                                                                        NVKELQSLENQLETSLRGVRAKKDHLLIDEIHDLNRKASLFHQENTDLYNKINLIRQEND
                                                                                                                                                                                                           MKSVIDRYGKAKEEQQ----VVANPNSELKFWQREAASLRQQLHNLQENYRQLTGDDLSGL 118
                                                                                                                                                                                                                                         GRGKIEIKRIENTINRQVTFCKRRNGLLKKAYELSVLCDAEVALIVFSSRGRLYEYSNNS
                                                                                                                                                                                                                                                                                                     102;
                                                                                    ELHKKIYETEGPSGVNRESPTPFNFAVVETRDVPVQ----LELSTLPQQNNIEPSTA---
                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                      Conservative
284
                                                                                                                                                                                                                                                                                                                     35.1%;
41.1%;
                                                                                                                                                                                                                                                                                                     49;
                                                                                                                                                                                                                                                                                                Score 426.5; DB IV,
Pred. No. 5.1e-22;
                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                              Length
                                                                                                                                                                                                                                                                                                                                   284;
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                                       The present invention provides the protein and coding sequences of the dea mays ZmWADS2 protein, which is specifically expressed in pollen. The sequences can be used to produce male Sterile plants, as ZmWADS2 is essential for pollen tube growth. These are useful in hybrid breeding, particularly of corn, cereal and grain. The present sequence is the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel nucleic acid molecule useful for cloning and expressing a pollen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SMKSVIDRYGKAKEEQQVVANPNSELKFWQREAASLRQQLHNLQENYRQLTGDDLSGLNV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HKKIYETEGPSGVNRESPTPFNPAVVETRDVPVQLELSTLPQQNNIEPSTAPKLGLQLIP 240
                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                   121 KELQSLENQLETSLRGVRAKKDHLLIDEIHDLNRKASLFHQENTDLYNKINLIRQENDEL
                                                                                                                                                                                                                                                                                                                                                                                                      1 MGRGKIVIRRIDNSTSRQVTFSKRRNGIFKKAKELAILCDAEVGLVIFSSTGRLYEYSST
                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4ADS box gene; ZmMAD52; pollen-specific expression; development; function; transgenic plant; male sterility;
                                                                                                                                                                                                                                                                                                                 Length 240;
                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                      100.0%; Score 1216; DB 22; 100.0%; Pred. No. 3.5e-102;
                                                                                                                                                                                                                                                                                                                                                                ;
0
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                                                                                                                                                                                                                                                                                                                                                        .0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Schreiber D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 1; Page 56-57; 66pp; English.
Claim 1; Page 66-67; 76pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Maize ZMMADS2 protein, SEQ ID NO:2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAB73333 standard; Protein; 1240 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (SUED-) SUEDWESTDEUTSCHE SAATZUCHT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Maize MADS box gene; ZmMAD$2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16-AUG-2000; 2000WO-EP08002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99EP-0116268
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2001-211214/21.
N-PSDB; AAF76058, AAF76068
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22-MAY-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                        Matches 240; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Loerz H, Dresselhaus T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hybrid seed production.
                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                              Sequence 240 AA;
                                                                                                                                                                         ZmMADS2 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200112799-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18-AUG-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAB73333;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Zea mays.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  pollen
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                                            their use in the generation of transgenic plants. The ZmWADS2 regulatory sequences are useful for cloning and expressing a pollen-specific or pollen-abundant gene in a plant, and may also be used to drive the expression of a gene of interest in a pollen-specific or pollen-preferred manner. The ZmWADS2 regulatory sequences are useful for isolating related regulatory sequences are useful for isolating related specificity to genes of other plant species which confer pollen or group sequences are useful in plant breeding, especially for the production of hybrid seed. In particular, they may be used to drive the production of hybrid seed. In particular, they may be used to drive the pollen-specific expression of heterologous genes which confer nuclear or cytoplasmic male
that it has an essential role in pollen development and function, in particular in pollen tube growth. The invention also relates to vectors and host cells comprising the ZmMADS2 regulatory or genomic sequence, an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          promoter;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 SMKSVIDRYGKAKEEQQVVAANPNSELKFWQREAASLRQQLHNLQENYRQLTGDDLSGLNV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 KELQSLENQLETSLRGVRAKKDHLLIDEIHDLNRKASLFHQENTDLYNKINLIRQENDEL 180
                                                                                                                                                                                                                    sterility in transgenic plants (e.g., cereals). The present sequence
                                                                                                                                                                                                                                                                                                                                                                                                     1 MGRGKIVIRRIDNSTSRQVTFSKRRNGIFKKAKELAILCDAEVGLVIFSSTGRLYEYSST 60
                                                                                                                                                                                                                                                                                                                                                      ;
0
                                                                                                                                                                                                                                                                                                                  100.0%; Score 1216; DB 22; Length 240; 100.0%; Pred. No. 3.5e-102; Live 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Arabidopsis thaliana protein fragment SEQ ID NO: 37350.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAG31142 standard; Protein; 228 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99US-0127462.
99US-0128234.
99US-0128714.
                                                                                                                                                                                                                                represents ZmMADS2 protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99US-0121825
99US-0123180
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99US-0126785
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                                                                                                                                                                                                                                                                                                                                 Best_Local Similarity 100.0
Matches 240; Conservative
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                                                                                                                                                                                                                                                                   240 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17-0CT-2000
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25-MAR-1999;
29-MAR-1999;
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16-APR-1999;
19-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25-FEB-1999;
05-MAR-1999;
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                                                                                                                                                                                                                                                                     Sequence
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99US-0129845 99US-0130077

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Novel nucleic acid molecule, ZmMADS2 derived from pollen of Zea mays useful for cloning and expressing a pollen specific sequence in a plant and for producing male sterile plants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16-AUG-2000; 2000WO-EP08001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Maize ZmMADS2 SEQ ID NO: 2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Loerz H, Dresselhaus T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2001-211213/21.
N-PSDB; AAF76445.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT
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Amino acid sequenc
Poplar PTAG-1 flor
Amino acid sequenc
Eucalyptus grandis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Maize ZmMADS2 SEQ
Maize ZmMADS2 prot
Arabidopsis thalia
Arabidopsis thalia
Arabidopsis thalia
Arabidopsis thalia
                                                                                                              (without alignments)
432.404 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /SIDSI/gcgdata/geneseq/geneseqp-embl/AA1983.DAT:*
/SIDSI/gcgdata/geneseq/geneseqp-embl/AA1984.DAT:*
/SIDSI/gcgdata/geneseqy-embl/AA1985.DAT:*
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/SIDSI/gcgdata/geneseqy-embl/AA1993.DAT:*
                                                                                                                                                                                                1 MGRGKIVIRRIDNSTSROVT......PQQNNIEPSTAPKLGLQLIP 240
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                                                                                             August 11, 2002, 08:37:25 ; Search time 61.65 Seconds
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                    Total number of hits satisfying chosen parameters:
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AAG32045
AAG30615
AAG50753
AAY58657
AAB68438
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                                                                OM protein - protein search, using sw model
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Maximum DB seq length: 200000000
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Match Length DB
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assica floral	1332	19	253	ς.	393	44
sica floral	913	119	253	ς.	393	43
rALA1 gene pro	AAW43110	19	253	32.3	393	42
rassica olerace	32	19	253	ď.	393	41
mays	919	21	240	7	395.5	40
ucalyptus grandi	22	21	161	ď	96	39
s radiata tr	3331	21	181	ά.	398	38
$\mathcal{S}$	969	17	257	Э.	401	37
ŧ	963	17	251	3	401	36
S8 prot	LO.	20	248	3	401	35
nays protein	313	21	283	Э.	402	34
protei	313	21	260	Э.	402	33
nays protein	13	21	257	ω,	4	32
ta con	~	19	242	٠ ٣	402.5	31
thali	Į	21	248	'n	405	30
	AAW80999	20	248	ω.	405	29
Ų	S	21	268	3.	406	28
bidopsis thali	4	21	167	ω.	407	27
protein	~	21	262	Э.	412.5	26
protei	112	21	307	4	414	25
sis thali	258	21	258	4.	414	24
rotein	AAG34121	21	251	4		23
Arabidopsis AGL5 p	AAW81000	20	246	4	41	22
s thal	021	21	277	4	19.	21
s thali	AAG16689	21	277	4	6	20
s thali	)21	21	230	4	19.	19
s thali	69	21	230	4	6	18
Petunia nectary-sp	364	21	221	4	N	17
hybr	480	21	221	4.	42	16
Plant reproductive		21	222	4	424.5	15
nus radiata c	2	19	261	η.	42	14
ശ	AAG52721	21	300	5		13
Eucalyptus AGE-2 p	33	17	229	5	431	12

## ALIGNMENTS

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Male sterile plant; maize; hybrid breeding; pollen tube; ZmMADS2; grain; cereal; corn.
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AAB72888 standard; Protein; 240 AA.
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                                                                                                                                                                                       Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
                                                                                                                                                                                                                                  Arabidopsis thaliana protein fragment SEQ ID NO: 38587.
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                                                                                                                     06-SEP-2000
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99US-0123548.
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Arabidopsis thaliana

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       Protein identification; signal transduction pathway; metabolic hybridisation assay; genetic mapping; gene expression control; termination sequence.
                                         Arabidopsis
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                                                                                         AAG50753 standard; Protein; 238 AA.
                                                         18-OCT-2000
                                                                                                                                   228
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                                                                                                                                                                                                                                                                                                       Local Similarity es 135; Conserv
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                                                                                                                                 3 KLGLQL 238
:|||||
8 rlglql 233
                                                                                                                                                                                                  LHKKIY----ETEGPSGVNRESPTPFNFAVVETRDVPVQLELSTL---PQQNNIEPSTAP
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                                                                                                                                                                                                                                                                                                     52.3%;
nilarity 54.9%;
Conservative 4
                                         thaliana
                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                     99US-0157753
99US-0158029
99US-0158029
99US-0159294
99US-0159295
99US-0159330
99US-0159331
99US-0159638
99US-0159638
99US-0159638
99US-0160761
99US-0160767
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99US-0160769
99US-0160763
99US-0160763
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99US-0160763
99US-0160763
                                         protein fragment
                                                                                                                                                                                                                                                                                                     ; Score 636.5; DB 21; Length 234; 
; Pred. No. 1.1e-49; 
46; Mismatches 44; Indels 21;
                                         SEQ ID NO: 64351.
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                                                                                                                                                                                                                                                                                                       21;
                        pathway;
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 25-REB-1999
05-MAR-1999
09-MAR-1999
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16-APR-1999
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30-APR-1999
31-MAY-1999
31-JUN-1999
32-JUN-1999
33-JUN-1999
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33-JUN-1999
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990S-0121825
990S-0125788
990S-0125788
990S-0125789
990S-0126785
990S-01267462
990S-0130477
990S-013048
990S-0132485
990S-0132485
990S-0134219
990S-0134219
990S-0134219
990S-0134219
990S-0134218
990S-0134219
990S-0139452
990S-0139453
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RESULT
AAY58657
ID AAY5
XX
AC AAY5
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Best Local Similarity 54.0
Matches 135; Conservative
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14-OCT-1999

14-OCT-1999

14-OCT-1999

14-OCT-1999

18-OCT-1999

21-OCT-1999

21-OCT-1999

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28-OCT-1999
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16-SEP 1999
20-SEP 1999
22-SEP 1999
23-SEP 1999
24-SEP 1999
24-SEP 1999
04-OCT 1999
05-OCT 1999
07-OCT 1999
07-OCT 1999
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13-OCT-1999;
13-OCT-1999;
AAY58657;
                   AAY58657
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                                                             9 STAPKLGLQL 238
:|||||
2 ----rlglql 237
                                                                                                                                     ENDELHKKIY----ETEGPSGVNRESPTPFNFAVVETRDVPVQLELSTL---PQQNNIEP || :| || :| | |: :| eniklqkkvhgrtnaiegnssvdpisngtttya-----ppqlqliqlqpapreksi--
                  standard; Protein;
                                                                                                                                                                                                                                                                                       99US-0154018
99US-0154779
99US-0155139
99US-0155659
99US-0155659
99US-0157753
99US-0158029
99US-0158029
99US-0159294
99US-0159294
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99US-0160767
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                                                                                                                                                                                                                                                             52.1%;
54.0%;
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                   238
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es 45;
                                                                                                                                                                                                                                                                      DB 21;
                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                     Length
                                                                                                                                                                                                                                                                       238;
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ת הסיסי לי סיסי ת הסיסי לי סיסי לי מוד לי

30-JUN 1999
01-JUL 1999
01-JUL 1999
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19-JUL 1999
19-JUL

99US-0141287 99US-0142154 99US-0142055 99US-0142390 99US-0142920 99US-0143542 99US-0144085 99US-0144085 99US-0144085 99US-0144331 99US-0144333 99US-0144333 99US-0144333 99US-0144333 99US-0144333 99US-0144335 99US-014438 99US-0144593 99US-0145088 99US-0145086 99US-0145086

99US-0145918 99US-0145519 99US-0146386 99US-0147038 99US-0147038 99US-0147702 99US-0147703 99US-0147703 99US-0147703 99US-014773 99US-014773 99US-014871 99US-014881 99US-0148865 99US-0148723 99US-0148723 99US-0149723 99US-0150864 99US-0151088 99US-0151088

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Qy
                                                                                                                           В
                                                                                                                                                        QΥ
                           Ş
                                                              В
                                                                                                                                                                                                                                                                                                   The present sequence is that of the novel PTAG-2 protein of poplar (Populus balsamifera subsp. trichocarpa), as deduced from newly is closed gene and cDNA sequences (see AAZ57948-49). PTAG-2 is 1 cof 4 novel floral homeotic genes identified in this poplar species. It is a homologue of AGAMOUS and is expressed in floral tissues. PTAG-2 contains a MADS domain and a K-domain. The invention provides nucleic acid sequences of the 4 novel Populus genes, the corresponding cDNA sequences (see AAZ47942-49) and deduced amino acid sequences (see AAY58454-57). It also provides methods of using the corresponding cDNA sequences of the 4 novel Populus genes and cDNA sequences to produce genetically engineered Populus and other trees having modified fertility characteristics, including sterility. Genetic constructs useful in producing genetically centineered Populus and other trees include antisense versions of CPTAG-2, dominant negative mutants, and constructs useful for sense suppression. Sterile trees allow increased wood yield and a creduction in the production of allergens such as pollen.
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                                                                                                                                                                                           Matches
                                                                                                                                                                                                            Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Key
Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Domain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rottmann WH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     06-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      07-APR-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Poplar; PTAG-2; floral homeotic gene; transgenic plant; sterility;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Poplar PTAG-2 floral homeotic gene-encoded protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 31; Page 77; 92pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       characteristics such as sterility
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nucleic acid from Populus trichocarpa genes, useful f
transgenic plants, particularly trees, with modified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (UYOR-) UNIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  fertility.
                                                                                                                                                                                                                                                                         Sequence
 134
                                                                                                                               16
                                                                                                                                                          1 MGRGKIVIRRIDNSTSRQVTFSKRRNGIFKKAKELAILCDAEVGLVIFSSTGRLYEYSST 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2000-106662/10
                                                                                                                           lsvkelksleiklekgigrirskknellfaeieymqkr----eidlhnnnqllraki 186
                            LNVKELQSLENQLETSLRGVRAKKDHLLIDEIHDLNRKASLFHQENTDLYNKINLIR--- 174
                                                            svkstierykkacadssnngsvseanag--fyggeaaklrsgignlqnsnrnmlgeslsa
                                                                                           SMKSVIDRYGKA---KEEQQVVANPNSELKFWQREAASLRQQLHNLQENYRQLTGDDLSG 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  balsamifera subsp. trichocarpa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAZ57848, AAZ57949
                                                                                                                                                                                                                                                                             238
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                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OREGON HEALTH SCI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Brunner AM,
                                                                                                                                                                                                                                                                             ΑĄ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     98US-0080851
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    98CA-2227940
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    106.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "MADS domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                            35.6%;
46.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sheppard LA,
                                                                                                                                                                                          Score 433.5; DB z1;
pred. No. 2.9e-31;
"""matches 54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Strauss
                                                                                                                                                                                                                            DB 21; Length 238;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          useful for producing 
modified fertility
                                                                                                                                                                                               Indels
                                                                                                                                                                                                 19;
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RESULT
AAB68438
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                          Dр
                                                                                 Matches
                                                                                                          Query Match
                                                                                                 Best
                                                                                                                                                                             The present sequence represents a floral homeotic protein, designated pryAG-2, which is derived from Populus balsamifera subsp. trichocarpa. The specification also describes PTD, PTLF, and PTAG-1 proteins. The floral homeotic proteins are expressed in floral tissues. PTLF is a homologue of LEAFY (LFY) and FLORICAULA (FLO), and is expressed in immature inflorescences on which floral primordia are developing. PTD is a homologue of DEFICIENS (DEF), and is strongly expressed in stame primordia from the onset of organogenesis. PTAG-1 and PTAG-2 are homologues of AGAMOUS (AG). The floral homeotic proteins and polynucleotides are useful for producing transgenic plants having modified fertility characteristics, particularly sterility.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Floral homeotic gene;
LFY; FLORICAULA; FLO;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Amino acid sequence of the floral homeotic protein PTAG-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAB68438;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAB68438 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Populus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         02-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-APR-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          fertility; sterility.
                                                                                                                                                                                                                                                                                                                                                                                             Novel isolated polynucleotide derived from Populus species, useful for producing transgenic plants having modified fertility characteristic,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      175
                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                      Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB; AAF85400,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rottman WH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (UYOR-) UNIV OREGON HEALTH SCI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           187
                            16
                                                                                                 Local
                                                     1 MGRGKIVIRRIDNSTSRQVTFSKRRNGIFKKAKELAILCDAEVGLVIFSSTGRLYEYSST 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                œ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QENDELHKKIYETEGPSGVNRE--SPTPFN 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        aene--rkrqhmnlmpggvnfeimqsqpfd 214
                         {\tt lgrgkveikrienttnrqvtfckrrngllkkayelsvlcdaevalivfssrgrlyeysnn}
                                                                                                                                                                                                                                                                                                                                                                                                                                                          2001-336098/36
SMKSVIDRYGKA---KEEQQVVANPNSELKFWQREAASLRQQLHNLQENYRQLTGDDLSG
                                                                                                                                                                                                                                                                                                                                                      23; Page 62-63; 69pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               balsamifera
                                                                                                Similarity
                                                                                                                                                       238 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2000CA-2319853
                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Strauss SH, Brunner AM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99US-0410464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers 16..72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "MADS domain" 106..172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                entry)
                                                                                                 35.6%;
46.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PTD; PTLF; PTAG-1; PTAG-2; tl
DEFICIENS; DEF; AGAMOUS; AG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "K-domain"
                                                                                    39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         238
                                                                                   Score 433.5; DB
Pred. No. 2.9e-31
9; Mismatches 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PTAG-1; PTAG-2; floral tissue; LEAFY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sheppard LA;
                                                                                                               DB 22;
                                                                                      54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            transgenic plant;
                                                                                      Indels
                                                                                                                Length 238;
                                                                                       19;
                                                                                                                                                                                                                                              in stamen
                                                                                      Gaps
                                  75
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61

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(Populus balasmifera subsp. trichocarpa), as deduced from newly constant gene and cDNA sequences (see AAZ57946-47). PTAG-1 is 1 cof 4 novel floral homeotic genes identified in this poplar species. It is a homologue of AGAMOUS and is expressed in floral tissues. C PTAG-1 contains a MADS domain and a K-domain. The invention provides nucleic acid sequences of the 4 novel Populus genes, the c corresponding cDNA sequences (see AAZ47942-49) and deduced amino acid sequences (see AAZ47942-49) and deduced amino acid c sequences to produce genetically engineered Populus and other trees include antisense versions of c sterility. Genetic constructs useful in producing genetically c engineered Populus and other trees include antisense versions of c PTAG-1, dominant negative mutants, and constructs useful for sense c suppression. Sterile trees allow increased wood yield and a constructs useful in the production of allergens such as pollen.
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AAY58656
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Qγ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              B
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Sequence
                                                                                                                                                                                                                                                                                   The present sequence is that of the novel PTAG-1 protein of poplar
                                                                                                                                                                                                                                                                                                                       Claim 31; Page 67-68; 92pp; English.
                                                                                                                                                                                                                                                                                                                                                           characteristics such as sterility
                                                                                                                                                                                                                                                                                                                                                                        Nucleic acid from Populus trichocarpa genes, useful for producing transgenic plants, particularly trees, with modified fertility
                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rottmann WH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (UYOR-) UNIV OREGON HEALTH SCI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        06-APR-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CA2227940-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Domain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Poplar PTAG-1 floral homeotic gene-encoded protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11-APR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Populus balsamifera subsp. trichocarpa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Poplar: PTAG-1; floral homeotic gene; transgenic plant; sterility;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAY58656;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAY58656 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9
                                                                                                                                                                                                                                                                                                                                                                                                                                                  2000-106662/10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QENDELHKKIYETEGPSGVNRE--SPTPFN 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      svkstierykkacadssnngsvseanag--fyqqeaaklrsqignlqnsnrnmlgeslsa 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     aene--rkrqhmnlmpggvnfeimgsgpfd 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        lsvkelksleiklekgigrirskknellfaeieymqkr----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LNVKELQSLENQLETSLRGVRAKKDHLLIDEIHDLNRKASLFHQENTDLYNKINLIR---
                                                                                                                                                                                                                                                                                                                                                                                                                                AAZ57946,
241 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Brunner AM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    98US-0080851
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       98CA-2227940.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "MADS domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                  AAZ57947
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "K domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sheppard LA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Strauss SH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        --eidlhnnngllraki 186
                                                                                                                                               the
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AAB68437
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ъ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches 100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                     Novel isolated polynucleotide derived from Populus species, useful for producing transgenic plants having modified fertility characteristic,
                                                                                                                                             N-PSDB;
                                                                                                                                                                                Rottman WH,
                                                                                                                                                                                                       (UYOR-) UNIV OREGON HEALTH SCI
                                                                                                                                                                                                                               01-OCT-1999;
                                                                                                                                                                                                                                                      02-OCT-2000;
                                                                                                                                                                                                                                                                               01-APR-2001.
                                                                                                                                                                                                                                                                                                       CA2319853-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                         Floral homeotic gene;
LFY; FLORICAULA; FLO;
                                                                                                                                                                                                                                                                                                                                           Domain
                                                                                                                                                                                                                                                                                                                                                                  Domain
                                                                                                                                                                                                                                                                                                                                                                                                      Populus balsamifera.
                                                                                                                                                                                                                                                                                                                                                                                                                            fertility; sterility.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Amino acid sequence of the floral homeotic protein PTAG-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23-JUL-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAB68437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAB68437 standard; Protein; 241 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        178 DELHKKIYETEGPSGVNRES----STPFNFAVVETRDVPVQLELSTLPQQNNIEP----S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       134 lsvkelksleirlekgisrirskknellfaeieymqkr-----evdlhnnnqllraki 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            232 hqdqmalqlv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     230 TAPKLGLQLI 239
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16\ lgrgkveikrienttnrqvtfckrrsgllkkayelsvlcdaevalivfssrgrlyeysnd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MGRGKIVIRRIDNSTSRQVTFSKRRNGIFKKAKELAILCDAEVGLVIFSSTGRLYEYSST 60
                                                                                                                                          2001-336098/36.
DB; AAF85397, AAF85398, AAF85399.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             senerk--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SMKSVIDRYGKAKEEQQ----VVANPNSELKFWQREAASLRQQLHNLQENYRQLTGDDLSG 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       svkstierykkasadssntgsvseanaq--yyqqeaaklrsqignlqnsnrhmlgealss 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LNVKELQSLENQLETSLRGVRAKKDHLLIDEIHDLNRKASLFHQENTDLYNKINLIRQEN 177
                                                                                                                                                                              Strauss SH,
                                                                                                                                                                                                                                                      2000CA-2319853
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative 52; Mismatches
                                                                                                                                                                                                                               99US-0410464.
                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers 17..72
                                                                                                                                                                                                                                                                                                                              /note=
                                                                                                                                                                                                                                                                                                                                           106..
                                                                                                                                                                                                                                                                                                                                                     /note= "MADS domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     35.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                      PTD; PTLF;
DEFICIENS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         rqsmnlmpggadfeivqsq----pydsrnysqvnglqpashys
                                                                                                                                                                                                                                                                                                                              "K-domain"
                                                                                                                                                                                Brunner AM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 431.5; DB 2
Pred. No. 4.4e-31;
                                                                                                                                                                                                                                                                                                                                                                                                                                        PTAG-1; PTAG-2; floral tissue; LEAFY; DEF; AGAMOUS; AG; transgenic plant;
                                                                                                                                                                                Sheppard LA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      :: = = = ::
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         63;
                                                                                                                                                                                                                                                                                                                                                                                                                                     transgenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 241;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       35;
                                                                                                                                                                                                                                                                                                                                                                                                                                     plant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          231
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The present sequence represents a floral homeotic protein, designated PTAG-1, which is derived from Populus balsamifera subsp. trichccarpa. The specification also describes PTD, PTLF, and PTAG-2 proteins. The floral homeotic proteins are expressed in floral tissues. PTLF is a homologue of LEAFY (LFY) and FLORICAULA (FLO), and is expressed in

designated

Claim 23; Page 56-57; 69pp; English.

particularly sterility

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                     Plant; transcription factor; gene expression; eucalyptus; pine; acaci poplar; sweetgum; teak; mahogany; bZIP; G-box binding factor; basic heltx-loop-heltx zipper; homeotic; homeodomain; homeobox; MADS; homeodomain; zipper; LIM domain; AP2; EREBs; zinc finger domain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       immature inflorescences on which floral primordia are developing. PTD is a homologue of DEFICIENS (DEF), and is strongly expressed in stamer primordia from the onset of organogenesis. PTAG-1 and PTAG-2 are homologues of AGAMOUS (AG). The floral homeotic proteins and polynucleotides are useful for producing transgenic plants having
      New isolated polynucleotide encoding a plant transcription factor for producing a plant e.g. a woody plant, preferably eucalyptus or pine, having modified gene expression or modified activity of a polypeptide
                                                                                                                                                                                                                        09-MAR-2000;
                                                                                                                                                                                                                                                                                                              Eucalyptus grandis
                                                                                                                                                                                                                                                                                                                                                                                                                                Eucalyptus grandis transcription factor protein sequence #96.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25-JAN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAB32638 standard; Protein; 185
                                                                                                  Wood M,
                                                                                                                                                                            18-AUG-1999;
                                                                                                                                                                                          11-MAR-1999;
                                                                                                                                                                                                                                                     14-SEP-2000
                                                                                                                                                                                                                                                                                 WO200053724-A2
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                                                                      2000-579369/54
                                                                                                                                                                                                                                                                                                                                           2 Cys2His2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TAPKLGLQLI 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   lsvkelksleirlekgisrirskknellfaeieymqkr-----evdlhnnnqllraki 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DELHKKIYETEGPSGVNRES----PTPFNFAVVETRDVPVQLELSTLPQQNNIEP----S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LNVKELQSLENQLETSLRGVRAKKDHLLIDEIHDLNRKASLFHQENTDLYNKINLIRQEN 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             svkstierykkasadssntgsvseanag--yyqqeaaklrsqignlqnsnrhmlgealss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SMKSVIDRYGKAKEEQQ----VVANPNSELKFWQREAASLRQQLHNLQENYRQLTGDDLSG 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         lgrgkveikrienttnrqvtfckrrsgllkkayelsvlcdaevalivfssrgrlyeysnd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              senerk---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                             FLETCHER CHALLENGE FORESTS LTD.
                                                                                                                                              GENESIS RES & DEV CORP LTD
                                                                                                 McGrath A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         fertility characteristics, particularly sterility.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 241 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                        2000WO-US06112
                                                                                                                                                                          99US-0266513.
99US-0149485.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    241
                                                                                                                                                                                                                                                                                                                                           CCAAT box element; MYB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    35.5%;
40.0%;
                                                                                                  Shenk MA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          rqsmnlmpggadfeivqsq----pydsrnysqvnglqpashys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 431.5;
Pred. No. 4.4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                  Glenn M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    No. 4.4e-31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      63;
                                                                                                                                                                                                                                                                                                                                                                                                  eucalyptus; pine; acacia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 241;
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     RESULT 12
AAR99637
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           transcription factor. The transcription factor may be used to produce a plant having modified gene expression such as a woody plant e.g. a eucalyptus, pine, acacia, poplar, sweetgum, teak, or mahogany species or to modify the activity of a polypeptide in a plant. The transcription factors of the present invention are members from the following families of regulatory proteins: bZIP, bZIP family of G-box binding factors, basic helix-loop-helix zipper, homeotic/homeodomain/homeobox/MADS, homeodomain cipper, LIM domain, AP2 and EREBS, zinc finger domains of type 2
              Eucalyptus
                                            N-PSDB;
                                                                                                                                                                                                          30-MAY-1996
                                                                                                                                                                                                                                                                                                      Eucalyptus; reproductive gene; AGE2; Arabidopsis; agomous gene;
Antirrhinum; plena gene; sterility; fertility; forest tree;
                                                                                                                                                                                                                                                                                                                                                                         01-OCT-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cys2His2,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention relates to novel plant transcription factors from Eucalyptus grandis or Pinus radiata. The present sequence is one such
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim
                                                                                  Peacock
                                                                                                                                                     22-NOV-1994;
                                                                                                                                                                               22-NOV-1995;
                                                                                                                                                                                                                                     AU9539013-A
                                                                                                                                                                                                                                                              Eucalyptus globulus.
                                                                                                                                                                                                                                                                                         transgenic
                                                                                                                                                                                                                                                                                                                                              Eucalyptus AGE-2 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                               AAR99637 standard;
                                                                                                                          (CSIR ) COMMONWEALTH SCI & IND RES ORG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 179 qgn
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MGRGKIVIRRIDNSTSRQVTFSKRRNGIFKKAKELAILCDAEVGLVIFSSTGRLYEYSST
                                          1996-278411/29
DB; AAT34432.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QEN 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LNVKELQSLENQLETSLRGVRAKKDHLLIDEIHDLNRKASLFHQENTDLYNKI----NLIR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              mgrgkieikrienttnrqvtfckrrngllkkayelsvlcdaevalivfssrgrlyeysnn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    lsvkelkqlenrlergitrirskkhemllteieylqkkeielenesvflrtkiaevdriq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sirstierykkansdssntstvteinag--yyggesaklrggigmlgnsnrhlmgdslss 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SMKSVIDRYGKAKEEQ----OVVANPNSELKFWQREAASLRQQLHNLQENYRQLTGDDLSG 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8; Page 238; 747pp; English.
                                                                                 ES,
k wJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CCAAT box elements and MYB.
 reproductive
trees useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        185
                                                                                                                                                                                                                                                                                       plant; flower development; antisense; ribozyme
                                                                                               Harcourt RL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                               Southerton
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ā,
                                                                                                                                                     94AU-0009589
                                                                                                                                                                               95AU-0039013
                                                                                                                                                                                                                                                                                                                                                                                                                              Protein;
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50.3%;
  for es
                                                                                    S
                                                                                               Kyozuka J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    34;
 establishing
                                                                                                                                                                                                                                                                                                                                                                                                                                229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 431; DB 21; Pred. No. 3.4e-31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
useful for prodn. of sterile ablishing wood lot plantations
                                                                                               Llewellyn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 185;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          60
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Eucalyptus

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В
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Вþ
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25-FEB-1999
05-MAR-1999
09-MAR-1999
23-MAR-1999
25-MAR-1999
29-MAR-1999
01-APR-1999
01-APR-1999
016-APR-1999
116-APR-1999
119-APR-1999
21-APR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          its homology to the Arabidopsis agamous (AG) and Antirrhinum plena (PLE) flower development genes. AGE-2 shows 62% homology to AG and 64% homology to PLE protein. AGE2 is very highly expressed in anthers and flower buds. A related protein, AGE-1 (AAR99633), was also identified. Antisense or ribozyme constructs of AGE, or of FLE2 and SQE genes (see also AAT34426 and AAT34429-31), can be used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AGE-2 protein (AAR99637) is the product of a cDNA clone, AGE2 (AAT34432), isolated from Eucalyptus globulus cDNA on the basis of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Page 38-39; 60pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       re-forestation projects
                                                                                                                                                                                                         25-FEB-2000;
                                                                                                                                                                                                                                      06-SEP-2000
                                                                                                                                                                                                                                                                   EP1033405-A2
                                                                                                                                                                                                                                                                                            Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                         termination
                                                                                                                                                                                                                                                                                                                                        hybridisation
                                                                                                                                                                                                                                                                                                                                                      Protein identification; signal transduction pathway; metabolic pathway;
                                                                                                                                                                                                                                                                                                                                                                                 Arabidopsis thaliana protein fragment SEQ ID NO: 67050
                                                                                                                                                                                                                                                                                                                                                                                                              18-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAG52721 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   inflorescence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               produce sterile transgenic Eucalyptus trees by minimising
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               183
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MGRGKIVIRRIDNSTSROVTFSKRRNGIFKKAKELAILCDAEVGLVIFSSTGRLYEYSST 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LHKKIYETEG------PSGVNRESPTPFNFAVVETRD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             {\tt svkatierykkafsdsssgirseanvqfyqqesaklqqqinnmqnnnrqlvgdsiagmn}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    lrakiaesersqhadmnlmpggtnydfmqpsssqpfdsrn 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     mkdmktteqklekaiakirakknellfaeieymqkr----eidlhn-----nnqv 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SMKSVIDRYGKA-KEEQQVVANPNSELKFWQREAASLRQQLHNLQENYRQLTGDDLSGLN 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      229 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                         2000EP-0301439
                                                                                                                                                                                                                                                                                                                                     assay; genetic mapping; gene expression control; promoter;
                99US-0121825.
99US-0123180.
99US-0125788.
99US-0126786.
99US-0126786.
99US-0126785.
99US-0126787.
99US-0128714.
99US-0128714.
99US-0130077.
99US-01300479.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              49; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 431; DB 17; Length 229; Pred. No. 4.6e-31; Indels 29; Mismatches 57; Indels 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24;
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                     23-APR 1999
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06-MAY 1999
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11-MAY 1999
11-MAY 1999
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                                                                          16-JUN-1999
17-JUN-1999
18-JUN-1999
18-JUN
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                  9908-0130510
9908-013248
9908-013248
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9908-0140823
9908-0140823
9908-0143323
9908-0144332
9908-0144333
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99US-0144632. 99US-0144884. 99US-0144814. 99US-0145086. 99US-0145088.

990S-0145085.
990S-0145089.
990S-0145089.
990S-0145145.
990S-0145145.
990S-0145224.
990S-0145213.
990S-0145213.
990S-0145913.

S-0146386. S-0146388. S-0146389. S-0147038.

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27-OCT-1999
28-OCT-1999
28-OCT-1999
29-OCT-1999
24-FEB-1997;
23-SEP-1996;
04-OCT-1996;
13-FEB-1997;
                                                                                                        23-SEP-1997;
                                                                                                                                                                                                                                 Pinus radiata
                                                                                                                                                                                                                                                                      PrMADS3; cone-specific gene; radiata pine;
forest tree; timber; pulp; fibre; transgen.
                                                                                                                                                                                                                                                                                                                                     Pinus radiata
                                                                                                                                                                                                                                                                                                                                                                                28-AUG-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAW48623
                                                                                                                                                 02-APR-1998
                                                                                                                                                                                          WO9813503-A1
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293 dqtalqlv 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    126 vkgtierykkaisdnsntgsvaeinag--yyggesaklrggiisignsnrglmgetigsm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity 41.1 tes 102; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ELHKKIYETEGDSGVNRESPTPFNFAVVETRDVPVQ----LELSTLPQQNNIEPSTA---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MKSVIDRYGKAKEEQQ----VVANPNSELKFWQREAASLRQQLHNLQENYRQLTGDDLSGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                       cone-specific
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9905-0159584

9905-0160741

9905-0160770

9905-0160770

9905-0160814

9905-0160815

9905-0160815

9905-0160815

9905-0160880

9905-01619080

9905-0161404

9905-0161404

9905-0161405

9905-0161405

9905-0161405

9905-0161359

9905-0161359

9905-0161361

9905-0161361

9905-0161361

9905-0161920

9905-0161920

9905-0161923
    97US-0804879.
96US-0717971.
96AU-0002756.
97AU-0005092.
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41.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         49;
                                                                                                                                                                                                                                                                                                                                       PrMADS3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 426.5; DB 21; Length Pred. No. 1.7e-30; Mismatches 74; Indels
                                                                                                                                                                                                                                                                            transgenic
                                                                                                                                                                                                                                                                                                                                     protein.
                                                                                                                                                                                                                                                                            plant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           125
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RESULT 1
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This is the amino acid sequence of the PrMADS3 protein of Pinus radiata, deduced from an isolated cDNA clone (see AAV18012). Expression of PrMADS3 is restricted to male and female cones. The PrMADS1, 2 and 3 proteins (see also AAW48622 and AAW48623) have been expressed in E. coli and characterised as DNA binding proteins. Their DNA binding consensus sequence is similar to that of the ACAMOUS protein. All 3 proteins bind a Squence matching the consensus sequence of the CArG box. The invention relates to genes from reproductive tissues of Pinus radiata and Eucalyptus grandis and the use of the promoters (see AAV18013, AAV18015, AAV18017 and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAV18019-22) of such genes in expression cassettes used to modify a plant, especially a tree used in timber, pulp or fibre production, to increase vegetative growth and thus production of valuable material.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Method of enhancing vegetative growth in plant - comprises use of expression cassette containing heterologous coding region expressing product which aborts development
            17-MAR-2000; 2000WO-NZ00031
                                                                                                                                Plant promoter;
                                                                                                                                                            Plant reproductive tissue promoter protein.
                                                                                                                                                                                                                         AAB26795;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB;
                                          21-SEP-2000
                                                                      WO200055172-A1
                                                                                                     Pinus radiata.
                                                                                                                                                                                             22-JAN-2001
                                                                                                                                                                                                                                                   AAB26795 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Teasdale
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                                                                                                                                                                                                                                                                                                                           167 lqkklsetegrdvitgieqtsntntgtngpwdssitnt 204
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                                                                                                                                                                                                                                                                                                                                                                                                                      120
                                                                                                                                                                                                                                                                                                                                                                                                                                                   61
                                                                                                                                                                                                                                                                                    15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LHKKIYETEGP---SGVNRESPT----PFNFAVVET 208
                                                                                                                                                                                                                                                                                                                                                                                                                   VKELQSLENQLETSLRGVRAKKDHLLIDEIHDLNRKASLFHQENTDLYNKINLIRQENDE 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         mgrgrvqlrrienkinrqvtfskrrngllkkayelsvlcdaevaliifstrgklyefass 60
                                                                                                                                                                                                                                                                                                                                                                                     vkelqqlerqlevalthlrsrktqvmldqieelrqrerllh--
                                                                                                                                                                                                                                                                                                                                                                                                                                               smnktleryekcsyamqdttgvsdreaqnwhqevtklkgkvellqrsqrhllgedlgpln
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SMKSVIDRYGKAK-EEQQVVANPNSELKFWQREAASLRQQLHNLQENYRQLTGDDLSGLN 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1998-230712/20.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             261 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                         (first entry)
                                                                                                                                PrAG1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  35.0%;
40.8%;
                                                                                                                            reproductive tissue; transgenic plant; cereal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  44;
                                                                                                                                                                                                                                                      222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 425; DB 19;
Pred. No. 1.9e-30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                      A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 261;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
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                                                                                                                                                                                Qγ
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                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                          This invention relates to a novel plant promoter gene. The promoter is located in plant reproductive tissue, and the invention includes transgenic plants containing the promoter. The promoter can be used to produce plants which have a diminished reproductive capacity or which are sterile. The constructs can also be used to transform agronomically
                                                                                                                                                                                                                                                                                                                                               e.g. cereals, rice, maize, wheat, barley, oats, rye, soybean and The present sequence represents the protein encoded by the plant reproductive promoter (PrAG1) gene of the invention.
                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Figure 1; 51pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel plant reproductive tissue promoter, useful to produce plants which have a diminished reproductive capacity or which are sterile
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (CART-) CARTER HOLT HARVEY LTD.
(TASM-) TASMAN BIOTECHNOLOGY LTD.
(UNMT ) UNIV MICHIGAN TECHNOLOGICAL.
                                                                                                                                                                                                                                                                                                                                                                                                       important plants in which modulation of reproductive capacity (particularly the timing and abundance of flowering) is desirable.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB; AAA99362,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Podila GK, Liu J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17-MAR-1999;
 119
                                    118 LNVKELQSLENQLETSLRGVRAKKDHLLIDEIHDLNRKASLFHQENTDLYNKI 170
                                                                         61
                                                                                                            61
                                                                                                                                               1 mgrgkieikrienttnrqvtfckrrngllkkayelsvlcdaevalivfssrgrlyefanh 60
                                                                                                                                                                                  1 MGRGKIVIRRIDNSTSRQVTFSKRRNGIFKKAKELAILCDAEVGLVIFSSTGRLYEYSST 60
svkrtierykktcvdnnhggaisesnsq--ywqqeagklrqqidilqnanrhlmgdglta
                                                                                                          SMKSVIDRYGKAKEEQQ----VVANPNSELKFWQREAASLRQQLHNLQENYRQLTGDDLSG 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2000-594442/56
                                                                                                                                                                                                                       87;
                                                                                                                                                                                                                                                                                                                  222
                                                                                                                                                                  Conservative
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                                                                                                                                                                                                                                        34.9%; Score 424.5; DB 2 50.3%; Pred. No. 1.7e-30;
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Search completed: August 11, Job time: 3512 sec 2002, 09:35:57

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Database
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Maximum DB seq length: 2000000000
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4: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1983.DAT: *
4: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1984.DAT: *
5: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1984.DAT: *
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Gapop 10.0 , Gapext 1.0
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1280
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Listing first 45 summaries
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Copyright (c) 1993 - 2000 Comp
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Arabidopsis thalia	AAC42728	21	705	18.5	236.2	9
Maize ZmMADS2 gene	AAF76453	22	310	19.1	245	8
Maize MADS-box gen	AAF76066	22	310	19.1	245	7
Arabidopsis thalia	AAC43252	21	684	19.9	254.8	6
Arabidopsis thalia	AAC42918	21	687	20.8	265.6	5
Maize ZmMADS2 gene	AAF76455	22	5031	36.2	463.4	4
Maize MADS-box gen	AAF76068	22	5031	36.2	463.4	w
Maize ZmMADS2 codi	AAF76445	22	1268	86.7	1109.6	2
Maize MADS-box gen	AAF76058	22	1268	86.7	1109.6	
Description	ID		Query Match Length DB	Query	Score	Result No.
				,		

Novel nucleic acid molecule useful for cloning and expressing a pollen

Maize floral meris Zea mays AP1 gene.	AAT99437 AAV58307	18 19	1342 1345	10.4	133.6 133.6	4.4 5
A. thaliana larger	AAC84182	22	1368	0	134	43
Nucleotide sequenc	AAF80396	22	1134	10.5	134	42
<ol> <li>mays MADS-box p</li> </ol>	AAA51323	21	1015	0.	134	41
Zea mays DNA fragm	AAC43699	21	1267	0.	135.6	40
s g	AAC55901	21	1223	10.7	137	39
Zea mays DNA fragm	AAC43696	21	1178	0.	137.4	38
×	AAC35890	21	466	0.	138	37
us SC	AAT34429	17	1084	0.	138.4	36
mays DNA	AAC35822	21	434	0.	139.8	3 5
DNA	AAC44550	21	1494	11.0	141.2	34
Zea mays DNA fragm	AAC44058	21	1305	11.1	142	S S
~	AAV99860	20	959	11.1	142.2	32
	AAC43464	21	777	11.1	142.2	31
Arabidopsis thalia	AAC51039	21	903	11.1	142.4	30
Nucleotide sequenc	AAF85398	22	1219	11.1	142.6	29
Poplar floral home	AAZ57947	21	1201	11.1	142.6	28
Nucleotide sequenc	AAF85399	22	723	11.1	142.6	27
	AAZ35494	21	1157	11.4	146.2	26
hybri	AAZ50201	21	1157	1.	146.2	25
OSMADS1 cDNA. Ory	AAT14919	17	1143	11.7	149.4	24
Eucalyptus grandis	AAC56741	21	423	11.7	150	23
mays DNA	AAC47718	21	1321	11.8	150.8	22
Zea mays DNA fragm	AAC43678	21	1218	12.1	154.8	21
Nucleotide sequenc	AAF85401	22	1159	12.4	158.6	20
Poplar floral home	AAZ57949	21	1115	12.4		19
Nucleotide sequenc	AAF85402	22	714			18
Rice OsmADS6 cDNA.	AAV71739	20	1044			17
⋖	AAC57270	21	581	ω.		16
Plant PrAG1 promot	AAA99364	21	909	ω		15
Maize ZmMADS2 gene	AAF76454	22	251	13.6		14
Maize MADS-box gen	AAF76067	22	251	ω.	•	13
	AAT34432	17	997	4		12
9	9	21	706	14.7	188.4	11
Arabidopsis thalia	AAC50308	21	717	17.5		10

## ALIGNMENTS

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RESULT
AAF76058
WPI; 2001-211214/21.
P-PSDB; AAB73333.
                                                                                                                                                                    Maize MADS box gene; ZmMADS2; pollen-specific expression; pollen development; function; transgenic plant; male sterility; hybrid seed production; ss.
                                                                                                                                                                                                         Maize MADS-box gene ZmMADS2 cDNA,
                                                                                                                                                                                                                         22-MAY-2001 (first entry)
                                                                                                                                                                                                                                                               AAF76058 standard; cDNA; 1268
                                            Loerz H,
                                                                              18-AUG-1999;
                                                                                                16-AUG-2000; 2000WO-EP08002
                                                                                                                                   WO200112799-A2
                                                                                                                                                     Zea mays.
                                                            (SUED-) SUEDWESTDEUTSCHE SAATZUCHT.
                                          Dresselhaus T,
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                                           Schreiber D,
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             that it has an essential role in pollen development and function, in particular in pollen tube growth. The invention also relates to vectors and host cells comprising the zmmADS2 regulatory or genomic sequence, and their use in the generation of transgenic plants. The ZmmADS2 regulatory sequences are useful for cloning and expressing a pollen-specific or pollen abundant gene in a plant, and may also be used to drive the expression of a gene of interest in a pollen-specific or pollen-preferred manner. The ZmmADS2 regulatory sequences are useful for isolating related regulatory sequences of other plant species which confer pollen or group specificity to genes of interest operably linked to them. The regulatory sequences are useful in plant breeding, especially for the production of hybrid seed. In particular, they may be used to drive the pollen-specific expression of heterologous genes which confer nuclear or cytoplasmic male enteritity in transgenic plants (e.g., cereals). The present sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to regulatory elements (AAF76059-AAF76067) the maize MADS box gene ZmMADS2 (AAF76068) which are capable of expression in a pollen-specific manner. The ZmMADS2 protein (AABF) is expressed particularly in mature pollen after dehiscence, indicate the control of the contro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1268 BP; 360 A; 298 C; 303
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Novel nucleic acid mole useful for cloning and and for producing male

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Query Match
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The invention relates to regulatory elements (AAF76059-AAF76067) from the maize MADS box gene ZmMADS2 (AAF76068) which are capable of directing expression in a pollen specific manner. The ZmMADS2 protein (AAB7333) is expressed particularly in mature pollen after dehiscence, indicating that it has an essential role in pollen development and function, in particular in pollen tube growth. The invention also relates to vectors and host cells comprising the ZmMADS2 regulatory or genomic sequence, and their use in the generation of transgenic plants. The ZmMADS2 regulatory sequences are useful for cloning and expressing a pollen-specific or pollen-abundant gene of interest in a pollen-specific or pollen-preferred manner. The ZmMADS2 regulatory sequences are useful for isolating related regulatory sequences of other plant species which confer pollen or group
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   18-AUG-1999;
                                16-AUG-2000;
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                                                                                              WO200112798-A2
                                                                                                                                                           grain; cereal;
                                                                                                                                                                    Male sterile plant; maize; hybrid breeding; pollen tube;
                                                                                                                                                                                                       Maize ZmMADS2 gene SEQ ID NO:
                                                                                                                                                                                                                                       11-MAY-2001
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                            17-OCT-2000
                                                          AAC42918;
                                                                                     AAC42918 standard;
                                                                                                                                                           1938 ggtcggcctcgtcatcttctccagcaccggccgcctctacgagtactctagcaccag
                                                                                                                                                                                                                         1878 caagegeeggaaegggatetteaagaaggeeaaggagetegeeateetetgegatgegga 1937
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1583
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1525 ttcccctctcggctagcttcctc--ctctctccctcttcgtcttcctctttccttct 1582
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1465 atccgccctgcgccaagaaaagccatcgttcttcccacaaacgcacacatagaagcatca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention provides the protein and coding sequences of zea mays ZmMADS2 protein, which is specifically expressed in poll sequences can be used to produce male sterile plants, as ZmMADS2 essential for pollen tube growth. These are useful in hybrid bree particularly of corn, cereal and grain. The present sequence is p the ZmMADS2 coding sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel nucleic acid molecule, ZmMADS2 derived from pollen of Zea mays useful for cloning and expressing a pollen specific sequence in a plant of producing male sterile plants.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 5031 BP; 1555 A; 1006 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; Page 71-72; 76pp; English.
                                                                                                                                                                            485 ggtcggcctcgtcatcttctccagcaccggcctctacgagtactctagcaccag
                                                                                                                                                                                                                                                                                                                                                                              305
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                                                                                                                                                                                                                                                                                                   gaggggaaagalcgtgalccgcaggalcgalaactccacgagccggcaggtgaccttctc 424
                                                                                                                                                                                                                                                                                                                                                              tcgtcgtcggtccttgcttccgatcggagggccacaaccacaacctctcgctccatagcg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 agccgccctgcgccaagaaaagccatcgttcttcccacaaacgcacacatagaagcatca 65
                                                                                                                                                                                                                                                                                                                                            tgcgcgcgcgagccagggtcaagaagag----agctagctataggccggagatcgatggg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ttcccctctcggctagcttcttcctctctctccctcctcctcctcttcctc-ttcctc-124
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96.5%;
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Pred. No. 7.7e-114;
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4.

thaliana DNA fragment

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18.JUN-1999; 99US-0139455.  2 18.JUN-1999; 99US-0139456.  2 18.JUN-1999; 99US-0139458.  2 18.JUN-1999; 99US-0139458.  3 18.JUN-1999; 99US-0139461.  3 18.JUN-1999; 99US-0139462.  4 18.JUN-1999; 99US-0139463.  5 18.JUN-1999; 99US-013963.  6 18.JUN-1999; 99US-0139750.  7 18.JUN-1999; 99US-0139763.  8 21.JUN-1999; 99US-0139763.  8 21.JUN-1999; 99US-0139899.	25-FEB-2000: 2000EP-0301439.  25-FEB-1999: 99US-012180. 05-MAR-1999: 99US-012548. 05-MAR-1999: 99US-012568. 25-MAR-1999: 99US-012678. 25-MAR-1999: 99US-012678. 25-MAR-1999: 99US-012674. 29-MAR-1999: 99US-012674. 29-MAR-1999: 99US-012674. 29-MAR-1999: 99US-012674. 21-APR-1999: 99US-013044. 23-APR-1999: 99US-013044. 24-APR-1999: 99US-013044. 25-APR-1999: 99US-013044. 30-APR-1999: 99US-013044. 30-APR-1999: 99US-013044. 30-APR-1999: 99US-013048. 30-APR-1999: 9	Hybridisation assay; genetic mapping; gene expression control; protein identification; signal transduction pathway; metabolic pathway; promoter; termination sequence; ss. Arabidopsis thaliana.
17-AUG 20-AUG 20-AUG 20-AUG 20-AUG 23-AUG 23-AUG 25-AUG 25-AUG 27-AUG 27-AUG 27-AUG	PR 06-JUL-1999 PR 08-JUL-1999 PR 10-JUL-1999 PR 12-JUL-1999 PR 15-JUL-1999 PR 15-JUL-1999 PR 16-JUL-1999 PR 19-JUL-1999 PR 19-JUL-1999 PR 19-JUL-1999 PR 20-JUL-1999 PR 20-JUL-1999 PR 21-JUL-1999 PR 21-JUL-1999 PR 22-JUL-1999 PR 23-JUL-1999 PR 23-	PR 23-JUN-199 PR 23-JUN-199 PR 24-JUN-199 PR 28-JUN-199 PR 29-JUN-199 PR 01-JUL-199 PR 01-JUL-199 PR 02-JUL-199
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24-SEP-1999
29-SEP-1999
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07-SEP-1999;
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cacaacttgcaagaaaattatcggcagttgacgggagatgatctttctgggctgaatgtc
                                                                            agcatgaaatcagttatagatcggtacggcaaggccaaggaagagcagccagtcgtcgca
                                                                                                          gccgaggtcggtctcatcatcttctctagcaccggaaagctctatgactttgcaagctcc
                                                                                                                      gcggaggtcggcctcgtcatcttctccagcaccggccgcctctacgagtactctagcacc
                                                                                                                                                                ttctccaagcgccggaacgggatcttcaagaaggccaaggagctcgccatcctctgcgat
                                                                                                                                                                                               atgggaagagggaagattgtgatccaaaggatcgatgattcaacgagtagacaagtcact
                               aatcccaactcggagcttaagttttggcaaaggggaggcaagctagagcttgagacaacaactg
                                                                                                                                                     aaccccgcatcagaagtcaagttttggcagagagaagctgctgttctaagacaagaactg
                                                               agcatgaagtcggttattgatagatacaacaagagcaagatcgagcaacaacaactattg
                                                                                                                                                                                                                                           376;
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9908-0152363
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9908-0154039
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9908-0155486
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                                                                                                                                                                                                                                                               687;
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25-FEB 1999

05-MAR 1999

09-MAR 1999

23-MAR 1999

25-MAR 1999

06-APR 1999

06-APR 1999

16-APR 1999

11-APR 1999

21-APR 1999

23-APR 1999

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23-APR 1999

24-APR 1999

25-APR 1999

26-MAY 1999

06-MAY 1999

11-MAY 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                      Hybridisation assay; genetic mapping; gene expression protein identification; signal transduction pathway; metabolic pathway; promoter; termination sequence; ss.
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990S-0121825
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21-JUL-1999; 21-JUL-1999; 22-JUL-1999; 22-JUL-1999; 22-JUL-1999; 22-JUL-1999; 23-JUL-1999; 23-JUL-1999; 23-JUL-1999; 26-JUL-1999; 27-JUL-1999; 27-JUL-1999; 27-JUL-1999; 28-JUL-1999; 28-JUL-1999; 28-JUL-1999; 28-JUL-1999; 28-JUL-1999; 28-JUL-1999; 29-AUG-1999;	28 - MAY - 1999 03 - JUN - 1999 03 - JUN - 1999 04 - JUN - 1999 07 - JUN - 1999 10 - JUN - 1999 11 - JUN - 1999 16 - JUN - 1999 16 - JUN - 1999 18 - JUN - 1999 19 - JUL - 1999 19 - JUL - 1999 11 - JUL - 1999 12 - JUL - 1999 13 - JUL - 1999 14 - JUL - 1999 15 - JUL - 1999 16 - JUL - 1999 17 - JUL - 1999 18 - JUL - 1999 18 - JUL - 1999 19 - JUL - 1999	24-MAY-1999; 25-MAY-1999; 27-MAY-1999;
99US -0145086 99US -0145088 99US -0145087 99US -0145089 99US -0145192 99US -0145145 99US -0145218 99US -0145218 99US -0145218 99US -0145218 99US -0145218 99US -0145218 99US -0145318 99US -0145918 99US -0145918 99US -0145918 99US -0145918	990S-0136782 990S-0137522 990S-0137523 990S-0137502 990S-0138094 990S-0138047 990S-0139452 990S-0139453 990S-0139455 990S-0139455 990S-0139456 990S-0139461 990S-0139461 990S-0139461 990S-0139462 990S-0139462 990S-0139463 990S-0139463 990S-0139463 990S-0140823 990S-0140823 990S-0140823 990S-0140823 990S-0142803 990S-0142803 990S-0142803 990S-0142803 990S-0142803 990S-0144085 990S-0144333 990S-0144333 990S-0144333 990S-0144333 990S-0144333 990S-0144333 990S-0144333 990S-0144333 990S-0144333 990S-0144333 990S-0144333 990S-0144333 990S-0144333 990S-0144332 990S-0144332 990S-0144332 990S-0144332	99US-0135629. 99US-0136021. 99US-0136392.
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	9908-0147302 9908-0147722 9908-0147733 9908-0147733 9908-0148771 9908-014871 9908-014874 9908-014972 9908-014972 9908-014972 9908-014972 9908-014972 9908-015066 9908-015066 9908-015106 9908-015106 9908-015106 9908-015106 9908-015106 9908-015106 9908-0151753 9908-0154018 9908-0154018 9908-0156458 9908-0157753 9908-015869 9908-0158869 9908-0158869 9908-0158869 9908-0158869 9908-0158869 9908-0158869 9908-0158869 9908-0158869 9908-0158869 9908-0158869 9908-0159289 9908-0159289 9908-0159299 9908-0159299 9908-0159299 9908-0159293	21

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RESULT
AAF76066
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28-OCT-1999;
29-OCT-1999;
                                                                                                                   Zea mays
                                                                                                                                                         Maize MADS box gene; ZmMADS;
pollen-specific expression;
                                                                                                                                                                                              Maize MADS-box gene
                                                                                                                                              function;
             18-AUG-1999;
                                                                                          WO200112799-A2
                                                                                                                                                                                                                           22-MAY-2001
                                                                                                                                                                                                                                                    AAF76066;
                                     16-AUG-2000;
                                                                22-FEB-2001
                                                                                                                                                                                                                                                                            AAF76066 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gcggaggtcggcctcgtcatcttctccagcaccggccgcctctacgagtactctagcacc
                                                                                                                                                                                                                                                                                                                                             tacaagaaggettatggaacgtcgaacacaaatggatt 578
                                                                                                                                                                                                                                                                                                                                                            cataaaaagatatatgagactgaaggaccaagtggagt 937
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                                                                                                                                              transgenic
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                                     2000WO-EP08002
                                                                                                                                                                                                                          (first
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99US-0161993.
99US-0162142.
             99EP-0116268
                                                                                                                                                                                                                                                                              DNA;
                                                                                                                                                                                                 ZmMADS2 5'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19.9%;
65.1%;
                                                                                                                                             plant;
                                                                                                                                                                       ZmMADS2;
                                                                                                                                           regulatory element; pollen development;
male sterility; hybrid seed production;
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                                                                                                                                                                                                                                                                            ВP
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Pred. No. 2.
                                                                                                                                                                       promoter;
                                                                                                                                                                                                 UTR, SEQ ID NO:10
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                                                                                                                                                                     5' untranslated region; 5' UTR;
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Sequence 310 BP;

51

A; 112 C; 68 G; 79 T; 0 other;

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sequences are useful for cloning and expressing a pollen-specific or pollen-abundant gene in a plant, and may also be used to drive the expression of a gene of interest in a pollen-specific or pollen preferred manner. The ZmMADS2 regulatory sequences are useful for isolating related regulatory sequences of other plant species which confer pollen or group specificity to genes of interest operably linked to them. The regulatory sequences are useful in plant breeding, especially for the production of hybrid seed. In particular, they may be used to drive the pollen-specific expression of heterologous genes which confer nuclear or cytoplasmic male sterility in transgenic plants (e.g., cereals). The present sequence represents the ZmMADS2 gene 5' untranslated region (5' UTR).
                                                                                                                                                                                                                                                                                             The invention relates to regulatory elements (AAF76059-AAF76067) from the maize MADS box gene ZmMADS2 (AAF76068) which are capable of directing expression in a pollen-specific manner. The ZmMADS2 protein (AAR73333) is expressed particularly in mature pollen after dehiscence, indicating that it has an essential role in pollen development and function, in particular in pollen tube growth. The invention also relates to vectors and host cells comprising the ZmMADS2 regulatory or genomic sequence, and their use in the generation of transgenic plants. The ZmMADS2 regulatory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     specific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel nucleic acid molecule useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (SUED-) SUEDWESTDEUTSCHE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     plant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Schreiber D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cloning and expressing a pollen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Heuer
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Query Match Best Local Matches 179 119 223 163 104 59 44 cctcctcttcctc-ttcctcccttcgggaaacctgctgcctttgagctttcttcttcg 162 agaaagatagatcccgccatcgtcgtcgtcggtccttgcttccgatcggagggccacaac aaacgcacacatagaagcatcattcccctctcggctagcttcctc--ctctctccctcct agatagatagatecegecategtegteg-eegteettgetteegateggagggeeacaae cttcgtcttcctcttccttctcccttgggaaacctgctgcctttgagctttcttcttcg 285; Similarity Conservative 19.1%; 95.3%; 0; Score 245; DB 22; Pred. No. 8.1e-56; Mismatches 10; Length 310; Indels 4; Gaps 178 222 58 ω

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RESULT
AAF76453
ID AAF7
OS XX
Zea mays
                  grain; cereal;
                         Male sterile plant; maize;
                                          Maize ZmMADS2 gene fragment SEQ ID NO: 10.
                                                             11-MAY-2001
                                                                               AAF76453;
                                                                                                 AAF76453 standard; DNA; 310
                                                                                                                 œ
                                                              (first entry)
                  corn;
                         hybrid breeding; pollen
                           tube;
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Qy 밁 QΥ Вb Qy 밁 Qy Вþ

Вр

238 283

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ARCSULT
AAC42728
ID AAC4
XX Hybr
KW Prott
KW Meta
XX Meta
XX Meta
XX Arab
XX Arab
                                                                                                                                                                                                                                                                                   Qγ
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Best Local S
Matches 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention provides the protein and coding sequences of the Zea mays ZmMADS2 protein, which is specifically expressed in pollen. The sequences can be used to produce male sterile plants, as ZmMADS2 is essential for pollen tube growth. These are useful in hybrid breeding, particularly of corn, cereal and grain. The present sequence is part of the ZmMADS2 coding sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel nucleic acid molecule, 2mMADS2 derived from pollen of Zea mays useful for cloning and expressing a pollen specific sequence in a plant and for producing male sterile plants \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 310 BP; 51 A; 112 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Loerz
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                                                      Hybridisation assay; genetic maprotein identification; signal
                                                                                                                                                               AAC42728 standard; DNA; 705
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (SUED-) SUEDWESTDEUTSCHE SAATZUCHT
                       Arabidopsis thaliana
                                                                                           Arabidopsis thaliana DNA fragment SEQ ID NO: 36632.
                                                                                                                17-OCT-2000 (first entry)
                                            metabolic pathway; promoter; termination sequence;
                                                                                                                                                                                                                                                                                                                119
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                                                         genetic mapping; gene expression control;
on; signal transduction pathway;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Schreiber D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 245; DB 22;
Pred. No. 8.1e-56;
0; Mismatches 10;
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                                               SS
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   25-FEB-1999
05-MAR-1999
09-MAR-1999
23-MAR-1999
24-MAR-1999
01-APR-1999
01-APR-1999
01-APR-1999
01-APR-1999
23-APR-1999
24-MAY-1999
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99US-0127462.
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S-0141842.
S-0142154.
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28-SEP-1999;
04-OCT-1999;
05-OCT-1999;
06-OCT-1999;
07-OCT-1999;
13-OCT-1999;
13-OCT-1999;
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                                                                                 atggggaggggaaagatcgtgatccgcaggatcgataactccacgagccggcaggtgacc
aagaaggaccatctcttgatagatgagattcacgatttgaatcgaaaggcaagtttattt
                         gtcaaagaactgcagtccctggagaatcaattggaaacaagcctgcgtggtgtccgcgca
                                                          ctgcacaacttgcaagaaaattatcggcagttgacgggagatgatctttctgggctgaat
                gctaacgacctacaaaaccttgaagaccagctagtaacaagtctaaaaggtgttcgtctc
                                                 tcaagtatgaaaacaatcattgagcggtacaacagagtaaaagaggagcagcatcaactt
                                                                                                                             -ccagcatgaaatcagttatagatcggtacggcaaggccaaggaagagcagcaagtcgtc
                                                                                                                                                                                                                        atggggagaggaagatagttatacgaaggatcgataactctacaagtagacaagtgact
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                                                                                                                                                                                                                                                         Similarity 63.
74; Conservative
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9908-0155458
9908-0156458
9908-0157753
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Pred. No. 2.8e
0; Mismatches
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No. 2.
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25-FEB-1999
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11-MAY-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hybridisation assay; genetic mapping; gene expression control; protein identification; signal transduction pathway; metabolic pathway; promoter; termination sequence; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Arabidopsis thaliana.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    standard; DNA; 717 BP.
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Query Match
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Pred. No. 4.8e-50;
0; Mismatches 208;
           Indels
                                  Length
                                   717;
          15;
          Gaps
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         Wood
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RESULT 11
AAC55965
ID AAC559
                                  (GENE-)
                                                                                                                                                                                                                                                                                                           Plant; transcription factor; gene expression; eucalyptus; pine; poplar; sweetgum; teak; mahogany; baIF; G-box binding factor; basic helix-loop-helix zipper; homeotic; homeodomain; homeobox; homeodomain zipper; LIM domain; AP2; EREBs; zinc finger domain; type 2 Cys2His2; CCAAT box element; MYB; ss.
                                                                                              11-MAR-1999;
18-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAC55965 standard;
                                                                                                                                                       09-MAR-2000; 2000WO-US06112
                                                                                                                                                                                              14-SEP-2000
                                                                                                                                                                                                                                     WO200053724-A2
                                                                                                                                                                                                                                                                        Eucalyptus grandis.
                                                                                                                                                                                                                                                                                                                                                                                                                               Eucalyptus grandis transcription factor DNA sequence #96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25-JAN-2001
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                                    GENESIS RES & DEV CORP LTD. FLETCHER CHALLENGE FORESTS LTD.
McGrath A,
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                                                                                              99US-0266513
99US-0149485
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Shenk MA,
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 706
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention relates to novel plant transcription factors from
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                                                                                                                                               ctgaatgtcaaagaactgcagtccctggagaatcaattggaaacaagcctgcgtggtgtc
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gagctcgaaaatgaaagtgtgttcctccgcacaaagat 663
                              ttatttcaccaagaaaatacagacttgtacaataagat 868
                                                                                                                                                                                               cagcagatccaaatgctgcaaaactccaacaggcacttgatgggtgattccttaagttca
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                                                               <u>aggtcaaagaagcatgagatgttattgactgagatcgagtacctgcagaaaaaagagatt</u>
                                                                                                                            ctctctgttaaggagctgaagcagctggaaaataggcttgaacgcggcatcacaaggatc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              364;
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57.1%;
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Pred. No. 1.9e-40;
""smatches 271;
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AAT34432
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                                                                                                                                                                                                                                                          globulus cDNA using primers based on homologous regions of the Arabidopsis and Antirrhinum genes, followed by a screening of a E. globulus library. It codes for a protein, AGE-2 (AAR99637), that shows homology to the AG and PLE proteins. AGE2 is strongly expressed in anthers and flower buds. Another cDNA clone, AGE1 (AAR34428), was also identified. Antisense or ribozyme constructs of AGE, or of FLE2 and SQE genes (see also AAR34426 and AAR34429-31), can be used to produce sterile transgenic Eucalyptus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eucalyptus; reproductive gene; AGE2; Arabidopsis; agomous gene; Antirrhinum; plena gene; sterility; fertility; forest tree; transgenic plant; flower development; antisense; ribozyme; ss.
                                                                                                                                                                                                                                                                                                                                                                               A cDNA clone (AAT34432), designated AGE2, is analogous to t Arabidopsis agamous (AG) and Antirrhinum plena (PLE) flower development genes. It was obtd. by PCR amplification of E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eucalyptus reproductive Eucalyptus trees useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30-MAY-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 8; Page 38-39; 60pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    re-forestation projects
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Peacock WJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (CSIR ) COMMONWEALTH SCI & IND RES
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                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                               trees by minimising inflorescence.
 471
                                                                                                    351 cggagatcgatggggaggggaaagatcgtgatccgcaggatcgataactccacgagccgg 410
                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1996-278411/29
DB; AAR99637.
ctctgcgatgcggaggtcggcctcgtcatcttctccagcaccggccgcctctacgagtac
                                          caggtgaccttctccaagcgccggaacgggatcttcaagaaggccaaggagctcgccatc 470
                                                                                   cagaggaaaatggggagggaaagatcgagatcaagcggatcgagaacacgacgaatcgg 136
                           caagtgactttctgcaagcggcggaatggcctcctcaagaaggcatatgaactctccgtt
                                                                                                                                              315;
                                                                                                                                                                                                                      997
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Southerton
                                                                                                                                              Conservative
                                                                                                                                                                                                                      BP;
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                                                                                                                                                                                                                      300 A; 211 C; 237 G;
                                                                                                                                                            14.0%;
60.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   genes - useful for prodn. of sterile for establishing wood lot plantations or \ensuremath{\mathsf{e}}
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                                                                                                                                                          Score 179.6;
Pred. No. 5.3
                                                                                                                                                Mismatches 204; Indels
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                                                                                                                                                                                                                      249 T; 0 other;
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                                                                                                                                                             5.3e-38;
                                                                                                                                                                           DB 17; Length 997;
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RESULT 1
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The invention relates to regulatory elements (AAF76059-AAF76067) from the maize MADS box gene ZmMADS2 (AAF76068) which are capable of directing expression in a pollen-specific manner. The ZmMADS2 protein (AAB7333) is expressed particularly in mature pollen after dehiscence, indicating that it has an essential role in pollen development and function, in particular in pollen tube growth. The invention also relates to vectors and host cells comprising the ZmMADS2 regulatory or genomic sequence, and their use in the generation of transgenic plants. The ZmMADS2 regulatory pollen-specific or pollen-abundant gene in a plant, and may also be used to drive the
                                                                                                                                                                    Claim 1; Page 60; 66pp; English.
                                                                                                                                                                                                     specific
                                                                                                                                                                                                                     Novel
                                                                                                                                                                                                                                                  WPI;
                                                                                                                                                                                                                                                                              Loerz H,
                                                                                                                                                                                                                                                                                                           (SUED-)
                                                                                                                                                                                                                                                                                                                                        18-AUG-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Zea mays.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Maize MADS box gene; ZmMADS2; 3' regulatory element; pollen-specific expression; pollen development; func
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Maize MADS-box
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                                                                                                                                                                                                                nucleic acid molecule useful for cloning and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           agtttatttcaccaagaaatacagacttgtacaataagatc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        attcgcgccaaaaagaatgagcttctatttgcggagattgagtatatgcaaaaaagggaa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gggctgaatgtcaaagaactgcagtccctggagaatcaattggaaacaagcctgcgtggt 767
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             agtagcgggatccgttctgaagctaatgttcagttttatcagcaagaatccgcaaagttg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gtcgtcgcaa---atcccaactcggagcttaagtttttggcaaagggaggcagcaagcttg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             tctagcaccagcatgaaatcagttatagatcggtacggcaaggccaaggaagagcagcaa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gggatgaatatgaaggatatgaagactactgagcaaaactagaaaaagcaatcgctaaa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ctttgcgaacgcgaggtcgccctcatcgtcttctccagtcgcggtcgcctctatgagtat 256
                                                                                                                                                                                                                                                                                                           SUEDWESTDEUTSCHE SAATZUCHT
                                                                                                                                                                                                     sequence
                                                                                                                                                                                                                                                                              Dresselhaus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          plant;
                                                                                                                                                                                                                                                                                                                                                                     2000WO-EP08002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                       99EP-0116268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         xpression; pollen development; function;
male sterility; hybrid seed production;
                                                                                                                                                                                                   in a plant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZmMADS2 3' regulatory element,
                                                                                                                                                                                                                                                                             Τ,
                                                                                                                                                                                                                                                                             Schreiber D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ВP
                                                                                                                                                                                                                                                                             Heuer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           expressing
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                                                                                                                                                                                                                a pollen
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Sequence 251 BP; 81 A;

27

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61

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82

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ZmMADS2

coding sequence.

The present invention provides the protein and coding sequences of the Zea mays ZmMADS2 protein, which is specifically expressed in pollen. The sequences can be used to produce male sterile plants, as ZmMADS2 is essential for pollen tube growth. These are useful in hybrid breeding, particularly of corn, cereal and grain. The present sequence is part of

The

of

Claim 2; Page 70; 76pp; English.

for producing male sterile plants

2001-211213/21.

Novel nucleic acid molecule, ZmMADS2 derived from pollen of Zea mays useful for cloning and expressing a pollen specific sequence in a pl

a plant

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QУ
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches 175;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      expression of a gene of interest in a pollen-specific or pollen-preferred manner. The ZmMANS2 regulatory sequences are useful for isolating related regulatory sequences of other plant species which confer pollen or group specificity to genes of interest operably linked to them. The regulatory sequences are useful in plant breeding, especially for the production of hybrid seed. In particular, they may be used to drive the pollen-specific expression of heterologous genes which confer nuclear or cytoplasmic male sterility in transgenic plants (e.g., cereals). The present sequence represents a ZmMADS2 gene 3' regulatory element.
                                                                                                                                                                                                                                                                                                                                                                                         Male sterile plant; maize; hybrid breeding; pollen tube; ZmMADS2; grain; cereal; corn; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1203 caaattaattttcagaccggaatggggtcgtggaattcagaggatgattgctttcta 1258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1143 actcagagaaagacatatttgtggcagggagatttgagatatgaacttataaatgtaatg 1202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Loerz H,
                                                                                                                                                                                                                                        (SUED-) SUEDWESTDEUTSCHE SAATZUCHT
                                                                                                                                                                                                                                                                  18-AUG-1999;
                                                                                                                                                                                                                                                                                          16-AUG-2000; 2000WO-EP08001
                                                                                                                                                                                                                                                                                                                 22-FEB-2001
                                                                                                                                                                                                                                                                                                                                          WO200112798-A2
                                                                                                                                                                                                                                                                                                                                                                                                                              Maize ZmMADS2 gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                       11-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAF76454;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAF76454 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 251 BP; 81 A; 27 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    caaataattttcagactggaatggggtcgtggaattcagaggatgattgctttcta 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  actcagagaaagacatatttgtggcagggagatttgagatatgaacttataaatgtaatg 120
                                                                                                                                                                                                                 Dresselhaus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                 99EP-0116267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                              fragment SEQ ID NO: 11.
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                                                                                                                                                                                                                Τ,
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                                                                                                                                                                                                               Schreiber D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ВP
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Pred.
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No. 6.6e-37
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                                                                                                                                                                                                                Heuer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1;
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RESULT 15
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                               Query Match
Best Local Sim:
Matches 306;
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches 175;
                                                                                                                       This invention relates to a novel plant promoter gene. The promoter is located in plant reproductive tissue, and the invention includes transgenic plants containing the promoter. The promoter can be used to produce plants which have a diminished reproductive capacity or which are sterile. The constructs can also be used to transform agronomically important plants in which modulation of reproductive capacity (particularly the timing and abundance of flowering) is desirable, e.g. cereals, rice, maize, wheat, barley, oats, rye, soybean and canola. The present sequence represents DNA encoding the plant reproductive promoter (PrAGI) of the invention.
                                                                                                                                                                                                                                                                                   Claim 8; Page 39-40; 51pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1203 caaataattttcagaccggaatggggtcgtggaattcagaggatgattgctttcta 1258
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                                                                                                   Sequence
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                                                                                                                                                                                                                                                                                                                                                           WPI; 2000-594442/56
                                                                                                                                                                                                                                                                                                                                                                                   Podila GK, Liu J, Karnosky DF,
                                                                                                                                                                                                                                                                                                                                                                                                              (CART-) CARTER HOLT HARVEY LTD.
(TASM-) TASMAN BIOTECHNOLOGY LTD.
(UNMT ) UNIV MICHIGAN TECHNOLOGICAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17-MAR-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200055172-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pinus radiata
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Plant promoter;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Plant PrAG1 promoter DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAA99364 standard; DNA; 909 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 caaataattttcagactggaatggggtcgtggaattcagaggatgattgctttcta 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       actcagagaaagacatatttgtggcagggagatttgagatatgaacttataaatgtaatg 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       actcagagaaagacatatttgtggcagggagatttgagatatgaacttataaatgtaatg 1202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               plant reproductive tissue promoter, useful to produce plants have a diminished reproductive capacity or which are sterile
                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                   909 BP;
                                Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2000WO-NZ00031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99NZ-0334715.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PrAG1; reproductive tissue; transgenic plant; cereal; ds
                                                                                                299 A; 172 C; 216 G; 222 T; 0 other;
                                          13.4%;
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                               0;
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Pred. No. 6.6e-37;
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                            Score 171.2; DB 2
Pred. No. 9.1e-36;
D; Mismatches 203
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                                                     DB 21; Length
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                               203;
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                             Indels
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Qγ
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481 atccaggagaatgagattcttcgcagcaagat 512
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                                                                                      aagaaggaccatctcttgatagatgagattcacgatttgaatcgaaaggcaagtttattt 836
                                                                                                                                                            gcaaatcccaactcggagcttaagtttttggcaaagggaggcagcaagcttgagacaacaa 656
                                                                                                                                                                                                                                                                                                                                                                            agcatgaaatcagttatagatcggtacggcaaggc---caaggaagagcagcaagtcgtc 596
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ttctgcaagcgccgaaatggtttattaaagaaggcgtatgaattatcagttctttgtgat 120
                                 caccaagaaaatacagacttgtacaataagat 868
                                                                  aaaaaagaacgagatgttgcttgaagagatcgacatcatgcagagaagggaacacatactt
                                                                                                                                        attaaggaactcaagcaacttgaggttcgacttgaaaaaggaatcagccgagtgcgatcc
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                                                                                                                                                                                                                              ctgcacaacttgcaagaaaattatcggcagttgacgggagatgatctttctgggctgaat
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Search completed: August 11, 2002, 08:42:14 Job time: 4354 sec

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OM nucleic - nucleic search, using sw model
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Sequence:
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DB seq length: 2000000000
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ADDRESSEE: Whinston, LLP STREET: One World Trade Center STREET: One World Trade Center STREET: 121 S.W. Salmon Street STREET: Portland STATE: Oregon COUNTRY: United States of America ZIP: 97204 COMPUTER READABLE FORM: MEDIUM TYPE: Disk, 3-1/2 inch COMPUTER: IBM PC compatible OPERATING SYSTEM: MS DOS SOFTWARE: WordPerfect 5.1 CURRENT APPLICATION NUMBER: U5/08/867,087B FILING DATE: June 2, 1997 CLASSIFICATION NUMBER: U.S. 08/323,449 FILING DATE: June 2, 1997 CLASSIFICATION NUMBER: U.S. 08/323,449 FILING DATE: June 7, 1995 ATPORNEY/AGENT INFORMATION: NAME: Dow, Alan. E. REGISTRATION NUMBER: 4630-47071 TELECOMMUNICATION INFORMATION: TELEPHONE: (503) 226-7391 TELEPHONE: (503) 226-7391 TELEPHONE: (503) 228-9446 INFORMATION FOR SEQ ID NO: 12: SEQUENCE CHARACTERISTICS: LENGTH: 1043 base pairs TYPE: nucleic acid STRANDEDNESS: double stranded TOPOLOGY: linear US-08-867-087B-12	ALIGNMENTS  EESULT 1  IS-08-867-087B-12  Sequence 12, Application US/08867087B  Patent No. 5990386  GENERAL INFORMATION: APPLICANT: An, Gynheung  TITLE OF INVENTION: GENES CONTROLLING FLORAL  TITLE OF INVENTION: AND APICAL DOMINANCE IN FLORAGE OF SEQUENCES: 70  CORRESPONDENCE ADDRESS: ADDRESSEE: Klarquist Sparkman Campbell Leic  ADDRESSEE: Klarquist Sparkman Campbell Leic	28 95 7.4 1062 4 US-09-105-652-1 29 95 7.4 1062 4 US-09-349-677-1 30 91.6 7.2 2679 3 US-08-904-284-4 31 91.4 7.1 5622 4 US-09-349-677-3 32 91.4 7.1 5622 4 US-09-349-677-3 33 90.4 7.1 1070 3 US-08-904-284-1 34 90.2 7.0 756 3 US-08-659-188-11 36 90.2 7.0 756 3 US-08-655-227-11 37 90.2 7.0 756 3 US-08-655-241-11 38 90.2 7.0 756 3 US-08-655-241-11 39 90.2 7.0 756 3 US-08-655-241-11 39 90.2 7.0 756 4 US-09-398-326-11 40 89.4 7.0 779 1 US-08-592-214A-9 41 89.4 7.0 779 3 US-08-655-241-9 42 89.4 7.0 779 3 US-08-655-241-9 43 89.4 7.0 779 3 US-08-655-241-9 44 89.4 7.0 779 3 US-08-655-241-9 45 89.4 7.0 779 3 US-08-655-241-9 47 89.4 7.0 779 3 US-08-655-241-9 48 89.4 7.0 779 3 US-08-655-241-9 49 89.4 7.0 779 3 US-08-655-241-9 49 89.4 7.0 779 3 US-08-655-241-9 40 89.4 7.0 779 3 US-08-655-241-9 41 89.4 7.0 779 3 US-08-655-241-9 42 89.4 7.0 779 3 US-08-655-241-9 43 89.4 7.0 779 3 US-08-655-241-9
	DEVELOPMENT LANTS	Sequence 1, Appli Sequence 4, Appli Sequence 3, Appli Sequence 3, Appli Sequence 11, Appli Sequence 11, Appli Sequence 11, Appli Sequence 11, Appl Sequence 11, Appl Sequence 11, Appl Sequence 11, Appl Sequence 9, Appli Sequence 9, Appli

Query Match

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Score 165.8;

DB 2;

Length 1043;

Best Local

Similarity

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                                                      ATTORNEY/AGENT INFORMATION: NAME: Dow, Alan. E.
TELECOMMUNICATION INFORMATION:
                                                                                                                                                    CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: GENE CONTROLLING FLORAL DETILE OF INVENTION: APICAL DOMINANCE IN PLANTS
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          REGISTRATION NUMBER: 35,123
REFERENCE/DOCKET NUMBER: 46:
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ZIP: 97204
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                                                                                                                                                                        SOFTWARE:
                                                                                                                                                                                         COMPUTER: IBM PC compatible OPERATING SYSTEM: MS DOS
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                                                                                                                                APPLICATION NUMBER: US/08/323,449B
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Best Local Similarity
GENERAL INFORMATION: APPLICANT: An, Gyr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (503) 228-9446 INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS: LENGTH: 1141 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
                                                                                                                                                              837 caccaagaaatacagacttgtacaataagatcaacctgattcgccaagaaaatg 891
                                                                                                                                               539
                                                                                                                                                                                                                                                                                                                         717
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LOCATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LOCATION: sequence of SEQ ID NO: IDENTIFICATION METHOD: Homology IDENTIFICATION METHOD: FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: nucleic acid STRANDEDNESS: double stranded
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LOCATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IDENTIFICATION METHOD: Homology to MADS-box proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY:
                                                                                                                                             CAAGATCTCAACAAAGACTTGAGGAAAAAGTTACAGGAAAACCAGTGCAGAGAATG
                                                                                                                                                                                                                                                                                                                                                           TTGAATTTCTTCAAACCACAC-AGAGAAATATTCTTGGTGAGGATTTGGGCCCACTAAGC 418
                                                                                                                                                                                                                                   aagaaggaccatctcttgatagatgagattcacgatttgaatcgaaaggccaagtttattt 836
                                                                                                                                                                                                                AGAAAGAACCAAGCACTGCTTGATCAGCTGTTTGATCTGAAGAGCAAGGAGCAACAGCTG
                                                                                                                                                                                                                                                                                      gtcaaagaactgcagtccctggagaatcaattggaaaccaagcctgcgtggtgtccgcgca 776
                                                                                                                                                                                                                                                                                                                                                                                          ctgcacaacttgcaagaaaattatcggcagttgacgggagatgatctttctgggctgaat 716
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ttctccaagcgccggaacgggatcttcaagaaggccaaggagctcgccatcctctgcgat 479
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  344;
                                                                                                                                                                                                                                                                                                                                                                                                                                GCAGCTCCAGAAAACGAAATTAATTACC----AAGAATACCTGAAGCTGAAAACAAGAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TCATGCATGTACAAAACCTTGGAGAGGTACCGCAGCTGCAACTACAACTCACAGGATGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    accagcatgaaatcagttatagatcggtacggcaaggccaaggcaagagcagcagtcgtc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GCCGAGGTCGCCCTCATCATCTTCTCCGGCCGCCGCCGCCTCTTCGAGTTCTCCAGCTCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Residues 90-143 of deduced amino acid sequence of SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MADS box
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57.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
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Pred. No. 4.4e-31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Dв 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  241;
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4.

TITLE OF INVENTION:

An, Gynheung

GENE CONTROLLING FLORAL DEVELOPMENT AND

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US-08-485-981-1
                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local :
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OPERATING SYSTEM: MS DOS SOFTWARE: WORDPERFECT 5.1 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REGISTRATION NUMBER: 35,123
REFERENCE/DOCKET NUMBER: 4630-42933
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE:
NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Disk, 3-1/2 inch
537 accagcatgaaatcagttatagatcggtacggcaaggcaaggaagagcaagtcgtc 596
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
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                                                                                                           480
                                                                                                                                                    125
                                                                                                                                                                   420 ttctccaagcgccggaacgggatcttcaagaaggccaaggagctcgccatcctctgcgat 479
                                                                                                                                                                                                                                                                                                                                             360 atggggagggaaagatcgtgatccgcaggatcgataactccacggagccggcaggtgacc 419
                                                                                                                                                                                                                         65 ATGGGGAGGGGAAGGTGGAGCTGAAGCGGATCGAGAACAAGATCAGCCGGCAGGTGACG 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: 08/323,449 FILING DATE: October 14, 1994 CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                  Match 11.7%;
Local Similarity 57.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: nucleic acid
STRANDEDNESS: double stranded
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08, FILING DATE: June 7, 1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: One World Trade Center
STREET: 121 S.W. Salmon Street
STREET: Suite 1600
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LOCATION: Residues 90-143 of deduced amino acid LOCATION: sequence of SEQ ID NO: 1: DENTIFICATION METHOD: Homology to MADS-box pro
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Portland
                                                                                   gcggaggtcggcctcgtcatcttctccagcaccggccgcctctacgagtactctagc---
                                                              GCCGAGGTCGCCCTCATCATCTTCTCCGGCCGCCGCCCCTCTTCGAGTTCTCCAGCTCA 244
                                                                                                                                           TTCGCCAAGCGCAGGAACGGCCTGCTCAAGAAGGCCCTACGAGCTCTCCCCTCCTGCGAC 184
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(503) 228-9446
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                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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TION METHOD: Homology to MADS-box proteins
TION METHOD: FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                               Score 149.4; DB 2; Pred. No. 4.4e-31;
                                                                                                                                                                                                                                                                                                                                                                                            Mismatches 241;
                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                              Length 1141;
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                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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TOPOLOGY: US-08-867-087B-1
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                                                                                                                                                                                                                                                           FILING DATE: 800
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: U.S. 08/323,449
FILING DATE: October 14, 1994
APPLICATION NUMBER: U.S. 08/485,981
TTTING DATE: June 7, 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1, Application Patent No. 5990386
                                                                                                                        TELEFAX: (503) 228-9446 INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: An, Gy
                                                                                                                                                                REFERENCE/DOCKET NUMBER: 46
TELECOMMUNICATION INFORMATION:
TELEPHONE: (503) 226-7391
                                                                                                                                                                                                                         FILING DATE: June 7, 1991
ATTORNEY/AGENT INFORMATION:
NAME: Dow, Alan. E.
REGISTRATION NUMBER: 35,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: An, Gynheung TITLE OF INVENTION: GEN TITLE OF INVENTION: AND
                                                                                                 SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
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                                   TYPE: nucleic acid
STRANDEDNESS: double stranded
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Whinston, LLP
ADDRESSEE: Whinston, LLP
STREET: One World Trade Center
STREET: 121 S.W. Salmon Street
STREET: Suite 1600
                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/867,087B
FILING DATE: June 2, 1997
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SOFTWARE: WordPer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Disk, 3-1/2 inch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY:
                                                                                LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          caccaagaaaatacagacttgtacaataagatcaacctgattcgccaagaaaatg 891
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AGAAAGAACCAAGCACTGCTTGATCAGCTGTTTGATCTGAAGAGCAAGGAGCAACAGCTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GCAGCTCCAGAAAACGAAATTAATTACC----AAGAATACCTGAAGCTGAAAACAAGAG 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gcaaatcccaactcggagcttaagttttggcaaagggaggcagcaagcttgagacaacaa 656
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TCATGCATGTACAAAACCTTGGAGAGGTACCGCAGCTGCAACTACAACTCACAGGATGCA 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Portland
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                                                                             1141 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      United States of America
                    linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                               sequence 6, Application US/08460512
Patent No. 5744693
                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                   APPLICANT: MEYEROWITZ
APPLICANT: YANOFSKY,
APPLICANT: MA, Hong
TITLE OF INVENTION: E
NUMBER OF SEQUENCES:
                               CLASSIFICATION: 800 PRIOR APPLICATION DATA:
                                                                                                       SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                            COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
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                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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FILING DATE:
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                                                                                                                                                                                                                                                                                                       Richard F. Trecartin
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                    US/08/293,278
                                                                                      US/08/460,512
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0; Mismatches 241; Indels
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                                                                                            Sequence 1, Application US/08460512 Patent No. 5744693
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Matches 291; Conserv
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INFORMATION FOR SEQ ID NO:
                                                           GENERAL INFORMATION:
APPLICANT: MEYERO
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LENGTH: 1125 base pairs
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TELECOMMUNICATION INFORMATION:
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NAME: Trecartin, Richard
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             APPLICANT: MA, Hong TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                               APPLICANT:
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LOCATION:
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STRANDEDNESS: single
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                                                                                                                                                                                               ACAACAACAATCAGTACCTGAGAGCAAAGAT
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110..853
                                              YANOFSKY, Martin F.
                                                                MEYEROWITZ, Elliot M.
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PLANTS HAVING
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; Pred. No. 1.2e:
0; Mismatches
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                 ALTERED FLORAL DEVELOPMENT
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CORRESPONDENCE ADDRESS:

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LENGTH: 1457 base pairs
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REFERENCE/DOCKET NUMBER: A-57322/RFT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION: NAME: Trecartin, Richard
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                                                                                                                                                                                                                                                                                                           686
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                                                                                                                                                                         543
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926 AAAGAGCTCAGGAACTTGGAAGGCAGATTAGAGAGAAGTATTACCCGAATCCGATCCAAG
                                                                                                                                                     806 GTGGCAGAAATTAATGCACAGTATTATCAACAAGAATCAGCCAAATTGCGTCAACAAATT
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LOCATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                           660 cacaacttgcaagaaaattatcggcagttgacgggagatgatctttctgggctgaatgtc 719
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn Release #1.0, Version #1.25
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                                    720 aaagaactgcagtccctggagaatcaattggaaacaagcctgcgtggtgtccgcgcaaag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Match 11.1%;
Local Similarity 57.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER:
                                                                                                                                                                                                                                                      atgaaatcagttatagatcggtacggcaaggcca---aggaagagcagcaagtcgtcgca 599
                                                                            ATCAGCATACAAAACTCCAACAGGCAATTGATGGGTGAGACGATAGGGTCAATGTCTCCC
                                                                                                                                                                                                                                GTAAAAGGTACTATTGAGAGGTACAAGAAGGCAATATCGGACAATTCTAACACCGGATCG
                                                                                                                                                                                                                                                                                                           GAAGTCGCACTCATCGTTTTCTCTAGCCGTGGTCGTCTCTATGAGTACTCTAACAACAGT 745
                                                                                                                                                                                                                                                                                                                             gaggtoggectegteatetteteeageaceggeetetaegagtaetetageaeeage 542
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TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Yanofsky, Martin F.
APPLICANT: Ferrandiz, Cristina
TITLE OF INVENTION: Seed Plants Characterized by Delayed
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TELECOMMUNICATION INFORMATION:
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ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
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                                                                                                                                        319 agggtcaagaagagatcagctagctataggccggagatcgatggggaggggaaagatcg 378
439 ggatcttcaagaaggccaaggagctcgccatcctctgcgatgcggaggtcggcctcgtca 498
                                          142 AGATAAAGAGGATAGAGAACACTACGAATCGTCAAGTCACTTTCTGCAAACGACGCAATG
                                                                379 tgatccgcaggatcgataactccacgagccggcaggtgaccttctccaagcgccggaacg 438
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                            OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: nucleic acid STRANDEDNESS: sing TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER:
                                                                                                                  82 AGGGTGGTGCGAGTAATGAAGTAGCAGAGAGGCAGCAAGAAGATAGGGAAGAGAGAAGATAG 141
                                                                                                                                                                                                              Local Similarity
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protein sequences."
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Pred. No. 3.6e-29;
0; Mismatches 248;
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US-09-349-677-7
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                                                 INFORMATION FOR SEO ID NO: SEQUENCE CHARACTERISTICS:
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                                                                                                   REFERENCE/DOCKET NUMBER: P-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
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STREET: 4,,
CITY: San Diego
CTATE: California
                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Yanofsky, N
APPLICANT: Ferrandiz,
TITLE OF INVENTION: Se
TITLE OF INVENTION: Se
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   STRANDEDNESS:
                     TYPE:
                                                                                                                                                    NAME: Campbell, Cathryn A REGISTRATION NUMBER: 31,8
                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC
OPERATING SYSTEM:
                                                                                         TELEFAX:
                                                                                                                                                                                                           FILING DATE
                                                                                                                                                                                                                                                           CLASSIFICATION:
                                                                                                                                                                                                                                                                             FILING DATE
                                                                                                                                                                                                                                                                                                                           SOFTWARE:
                                   LENGTH:
                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/09/349,677
                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE:
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                   nucleic acid
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                                                                                   (619) 535-8949
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                                                                                                                                                                                                                                                                                                                                                                                                                               United States
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                                                                                                                                                                                                                                                                                                                                                             IBM PC compatible
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single
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; Sequence 3, Applica ; Patent No. 5744693
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Best Local Similarity 54.8%;
                                                                                                  APPLICANT: MEYEROWITZ
APPLICANT: YANOFSKY,
APPLICANT: MA, Hong
TITLE OF INVENTION: F
                                                                                                                                                                               GENERAL INFORMATION:
                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: Richard F.
                                                                                      NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          499 tcttctccagcaccggcctctacgagtactctagcaccagcatgaaatcagttatag 558
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    322 AAAGGTACAAGAAAGCTTGCTCCGACGCCGTTAACCCCTCCGACCATCACCGAAGCTAATA 381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      559 atcggtacggcaaggc---caaggaagagcagcaagtcgtcgcaaatcccaactcggagc 615
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    439 ggatcttcaagaaggccaaggagctcgccatcctctgcgatgcggaggtcggcctcgtca 498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     142 AGATAAAGAGGATAGAGAACACTACGAATCGTCAAGTCACTTTCTGCAAACGACGCAATG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                319 agggtcaagaagagctagctagctataggccggagatcgatggggagggggaaagatcg 378
                  CITY:
                                STREET:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     304;
                  San Francisco
                                                                                                                                                                                                                 Application US/08460512
California
                                 4 Embarcadero Center,
                                                                                                                                                            MEYEROWITZ, Elliot M.
                                                                                                                                         YANOFSKY, Martin F.
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                                                                                                         PLANTS HAVING
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protein sequences."
                                                  Trecartin
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Pred. No. 3.6
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                                   Suite 3400
                                                                                                       ALTERED FLORAL DEVELOPMENT
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Best Local Similarity
Matches 278; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REGISTRATION NUMBER: 31,801
REFERENCE/DOCKET NUMBER: A-57322/RFT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08/460,512 FILING DATE:
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                                                                                                                                                  aaagaactgcagtccctggagaatcaattggaaacaagcctgcgtggtgtccgcgcaaag
                                                                                                                                                                                        ATCAGCATACAGAACTCGAACAGGCAATTGATGGGTGAGACGATTGGGTCAATGTCTCCC
                                                                                                                                                                                                                                                                                               aatcccaactcggagcttaagttttggcaaagggaggcagcaagcttgagacaaccagctg 659
                                                                                                                                                                                                                                                                                                                                            GTAAAAGGGACAATTGAGAGGTACAAGAAAGCAATATCGGATAATTCTAACACCGGATCC 416
                                                                                                                                                                                                                                                                                                                                                                                                                        GAAGTCGCACTCATTGTCTTCTAGCCGTGGCCGTCTCTATGAGTACTCAAACAACAGT 356
                                                                                                                                                                                                                                                                                                                                                                                                                                            TGCAAACGCAGAAATGGTTTGCTCAAGAAAGCTTACGAACTCTCTGTTCTTTGTGATGCT 296
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                                     aaggaccatctcttgatagatgagattcacgatttgaatcgaaaggcaagtttatttcac 839
                                                                                                              AAAGAGCTCAGGAACTTGGAAGGCAGATTAGACAGAAGTGTTAATCGAATCCGATCCAAG
                                                                                                                                                                                                                                                                   GTGGCAGAAATTAATGCACAGTATTATCAACAAGAATCTGCCAAATTGCGTCAACAAATT 476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1097 base pairs
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                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                       Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (619) 535-894
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 43, CONTROL STREET: San Diego CITY: San Diego CTATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Yanofsky, Martin F.
TITLE OF INVENTION: Cauliflower Floral Meristem Identify
TITLE OF INVENTION: Genes and Methods of Using Same
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: P-TELECOMMUNICATION INFORMATION: TELEPHONE: (619) 535-9001
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COMPUTER READABLE FORM:
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 317
                                                                                                                                   197
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                                                                                                                                                                                                                                                                                                                                                                       LOCATION: 1..1345
OTHER INFORMATION: /note= "product = Zea mays AP1"
                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: misc_feature LOCATION: 1..1345
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE:
                                                                                                                                                                                                                                                                                       Match 10.4%;
Local Similarity 57.5%;
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                                                                                 atcctctgcgatgcggaggtcggcctcgtcatcttctccagcaccggccgcctctacgag
                                                                                                                                 TACGCCACCGACTCCCGCATGGACAAAATTCTTGAACGCTATGAGCGATATTCCTATGCT
                   tactcta---gcaccagcatgaaatcagttatagatcggtacggcaaggccaaggaagag
                                                                 GTCCTCTGCGATGCCGAGGTCGCCGTCATCGTCTTCTCCCCCAAGGGCAAGCTCTACGAG
                                                                                                                                                 cggcaggtgaccttctccaagcgccggaacgggatcttcaagaaggccaaggagctcgcc 467
                                                                                                                                                                                                       GGCAACAAGGCGATGGGGGGGGGGAAGGTACAGCTGAAGCGGATAGAGAACAAGATAAAC 196
                                                                                                                                                                                                                                                                         300;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              nucleic acid
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N: 536
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                                                                             ; NAME/KEY: misc_feature
; LOCATION: 1.1345
; OTHER INFORMATION: /not
US-08-659-188-7
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   Matches 300;
                                 Query Match
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                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A
REGISTRATION NUMBER: 31,81
REFERENCE/DOCKET NUMBER: E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA:
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                                                                                                                                            FEATURE:
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                   Local Similarity
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                            LOCATION:
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                                                                                                                                                                                                                                        TYPE: nucleic acid
STRANDEDNESS: double
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Score 133.6; DB 3
Pred. No. 9.3e-27;
0; Mismatches 214
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                                     TELEPHONE: (619) 535-90 TELEFAX: (619) 535-8949 INFORMATION FOR SEQ ID NO:
                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-CTELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/655,227
FILING DATE: 05-JUN-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Yanofsky, Martin F.
TITLE OF INVENTION: Maize and Cauliflower APETALAI Gene
TITLE OF INVENTION: Products and Nucleic Acid Molecules
NUMBER OF SEQUENCES: 26
                 SEQUENCE CHARACTERISTICS:
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LENGTH:
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                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE:
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; NAME/KEY: misc_feature
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; OTHER INFORMATION: /note= "product = Zea mays AP1."
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                              STREET: 43.
STREET: 43.
CITY: San Diego
STATE: California
                                                                                                                                                    APPLICANT: Yanofsky, Martin F.
APPLICANT: Weigel, DetLef
TITLE OF INVENTION: Seed Plants Exhibiting Early Reproductive
TITLE OF INVENTION: Development and Methods of Making Same
COMPUTER READABLE FORM
                                                                                                                     CORRESPONDENCE ADDRESS:
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                                                                                                                                      NUMBER OF SEQUENCES:
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                                                                                                   ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GAAAAGGCTCTTATTTCAGCTGAATCTGAAAGTGAGGGAAATTGGTGCCACGAATACAGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ggccggagatcgatggggaggggaaagatcgtgatccgcaggatcgataactccacgagc 407
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                   92122
                                                                                   EE: Campbell and Flores
4370 La Jolla Village
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149..968
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Pred. No. 9.3e-27;
0; Mismatches 214;
                                                                                     Drive,
                                                                                     Suite
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
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Best Local Similarity 57.5%;
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,81
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             348 ggccggagatcgatggggagagggaaagatcgtgatccgcaggatcgataactccacgagc 407
                    821 aaaggcaagtttatttcaccaagaaaatacagacttgtacaa
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
616 GAAGGAGAGGTCACTGCAGGAGGAGAACAAGGCTCTGCAGAA
                                                                                                                                                                           701
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STRANDEDNESS: doub
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                                                                                                                                                                                                                                       aagcttgagacaacagctgcacaacttgcaagaaaattatcggcagttgacgggagatga
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                                                                   GAAGCACATCAGATCAAGGAAGAGCCACCTTATGGCCGAGTCTATTTCTGAGCTACAGAA 615
                                                                                                   gcgtggtgtccgcgcaaagaaggaccatctcttgatagatgagattcacgatttgaatcg
                                                                                                                                                            totttotgggotgaatgtoaaagaactgcagtcoctggagaatcaattggaaacaagoct
                                                                                                                                                                                                                                                                                      GAAAAGGCTCTTATTTCAGCTGAATCTGAAAGTGAGGGAAATTGGTGCCACGAATACAGG
                                                                                                                                                                                                                                                                                                                    cagcaagtcgtcgcaaatcccaactcggagcttaagt----tttggcaaagggaggcagc 640
                                                                                                                                                                                                                                                                                                                                                           TACGCCACCGACTCCCGCATGGACAAAATTCTTGAACGCTATGAGCGATATTCCTATGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  300;
                                                                                                                                           TCTAGAGTCTTTGAATCCCAAAGAGCTCCAGCAACTAGAGCAGCAGCTGGATAGCTCACT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (619) 535-8949
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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; LOCATION: 1..1345
; OTHER INFORMATION: /note= "product = Zea mays AP1"
US-09-149-976-7
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US-09-149-976-7
                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
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TELECOMMUNICATION INFORMATION:
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ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell & Flores LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: CDNA
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APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                     348 ggccggagatcgatgggggggaaagatcgtgatccgcaggatcgataactccacgagc 407
       585
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CTTY: San Diego
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH:
cagcaagtcgtcgcaaatcccaactcggagcttaagt----tttggcaaagggaggcagc 640
                                                                    tactcta---gcaccagcatgaaatcagttatagatcggtacggcaaggccaaggaagag 584
                                                                                                       GTCCTCTGCGATGCCGAGGTCGCCGTCATCGTCTTCTCCCCCAAGGGCAAGCTCTACGAG 316
                                                                                                                             atcctctgcgatgcggaggtcggcctcgtcatcttctccagcaccggccgcctctacgag 527
                                                                                                                                                                                                   | 0990a99f9accttctccaagcgcccggaacgggatcttccaagaaggcccaaggagctcgcc 467
                                                                                                                                                                                                                                                 GGCAACAAGGCGATGGGGGGGGGCGCAAGGTACAGCTGAAGCGGATAGAGAACAAGATAAAC 196
                                  TACGCCACCGACTCCCGCATGGACAAAATTCTTGAACGCTATGAGCGATATTCCTATGCT 376
                                                                                                                                                                             CGGCAGGTGACCTTCTCCAAGCGCCCGGAACGGCCTGCTCAAGAAGGCGCACGAGATCTCC 256
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                                                                                                                                                                                                                                                                                                                        Conservative
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; Patent No. 6355863
                                                                                                                                                                                                                                                          TELEFAX: (619) 535-89 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                  FEATURE:
NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                            MOLECULE TYPE:
                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: P-
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 05-JUN-1996 ATTORNEY/AGENT INFORMATION:
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             LOCATION: 1..1345
OTHER INFORMATION:
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CITY: San Diego
STATE: Californ
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OPERATING SYSTEM: PC-DOS/MS-DOS
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Reproductive Development and Methods of Making Same
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GAAGGAGAGGTCACTGCAGGAGGAGAACAAGGCTCTGCAGAA 657
                                                           GAAGCACATCAGATCAAGGAAGAGCCACCTTATGGCCGAGTCTATTTCTGAGCTACAGAA 615
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Search completed: August 11, 2002, 08:38:22 Job time: 10118 sec

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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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   Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
  569.4

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10216.440 Million cell updates/sec
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AW218280 EST303461

BE034403 WH04D03 W

BG592879 EST491557

AI974336 T110185e

BM323459 PIC1 19_E

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BE596704 PI1_58_DF

AL1389596 WHEC56A01

AW706936 SK08608 Y

BE445252 WHEL133_Y

AW184799 se82f12 Y

BE445264 HVSMEh008
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## ALIGNMENTS

BASE COUNT	source	FEATURES						COMMENT	JOURNAL		TITLE	AUTHORS	REFERENCE			ORGANISM	SOURCE	KEYWORDS	VERSION		DEFINITION	AW453286	RESULT 1
/organism="Zee mays" /cultivar="Ohio43" /db_xref="taxon:4577" /clone_lib="660 - Mixed stages of anther and pollen" /clone_lib="660 - Mixed stages of anthers to pollen shed" /clone_lib="660 - Mixed stages of anthers to pollen shed" /clone_lib="660 - Mixed stages of anthers to pollen shed" /clone_lib="660 - Mixed stages of anthers to pollen shed" /clone_lib="whole premieotic anthers to pollen shed" /dev_stage="premieotic anthers to pollen shed" /lab_host="xLOLR" /note="Organ: anthers; Vector: Lambda Zap; Site_1: EcoRI; Site_2: XhoI; Anther and pollen cDNA library. Directionally sequenced with 5' end at the EcoRI site. Created by Amise Franklin." 213 a 113 c 139 g 149 t	1614	Location/Qualifiers	nford	Fax: 650 725 8221	7) 1 m 10 (11 co) (11 ) 10 co)	STRIPTORY OF TAKEN DAIL ALTO CA 94304 TISA	Department of Biological Sciences	Contact: Walbot V	Unpublished (1999)	University	Maize ESTs from various cDNA libraries sequenced at Stanford	Walbot, V.	1 (bases 1 to 614)	Spermatophyta; Magnollophyta; Lillopsida; Poales; Poacede; PACC clade; Panicoideae; Andropogoneae; Zea.	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;	Zea mays	Zea mays.	EST.	AW453286.1 GI:6994072	mRNA sequence.	660039F01.y1 660 - Mixed stages of anther and pollen Zea mays cDNA,	611 by BONA	

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                                       Stanford University
855 California Ave, Palo Alto,
                                                                                                                                                                   Eukaryóta; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Zea.

1 (bases 1 to 608)
               Tel: 650 723 2227 Fax: 650 725 8221
                                                                          Department of Biological Sciences
                                                                                         Contact: Walbot
                                                                                                        Unpublished (1999)
                                                                                                                                                                                                                                                                                                       mRNA sequence.
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614044G10.y1 614 -
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walbot@stanford.edu
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                                                   mRNA sequence.
AI947410
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614044G10.x1 614 - root cDNA
Zea mays
                            EST.
            Zea mays.
                                        AI947410.1 GI:5739615
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/clone_lib="614 - roo"
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Eukaryota;

Viridiplantae;

Streptophyta; Embryophyta; Tracheophyta;

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VERSION
KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
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Plate: 614044 row: G col
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Department of Biological Sciences
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/clone_lib="614 - root cDNA library from
/tissue_type="root"
/dev_stage="3-4 days old"
/lab_host="%LOLR"
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Pred. No. 5.8e-52;
"'mmatches 6; Indels
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BE354988
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Department of Biological Sciences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Spermatophyta; Magnoliophyta; Liliopsida; Poales; clade; Panicoideae; Andropogoneae; Zea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: walbot@stanford.edu
Plate: 614073 row: H col
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 Sorghum bicolor
Eukaryota; Viri
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DG1_10_H09.b1_A002 Dark Grown
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35; Conservative
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650 725 8221
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/clone_lib="614 - root cDNA library from Walbot Lab"
/tissue_type="root"
/dev_stage="3-4 days old"
/lab_host="XLOLR"
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EcoRI; Site_2: XhoI; 3-4 days old root tissue
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      Eukaryota;
                      Solanum tuberosum
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                                               potato.
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Sequences have been trimmed to exclude PolyA, vector and regions
below Phred quality 16. The threshold for highest quality sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (2000)
Contact: Cordonnier-Pratt
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Department of Botany
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/clone_lib="Dark Grown 1 (DG1)"
/clone="Organ: 5-day-old dark-grown seedlings; Vector:
/note="Organ: 5-day-old jark-grown seedlings; Vector:
Lambda Zap; Site_l: XhoI; Site_2: EcoRI; The library was
made from poly-A RNA in the cloning vector lambda ZAP II.
Clones to be sequenced were prepared by mass excision."
a 125 c 138 g 88 t
                                                                                                                                  sequence.
                                                                                                                                                    potato roots Solanum 1
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    Viridiplantae;
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85.7%;
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Pred. No. 2.5e-34;
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Streptophyta; Embryophyta;
                                                                                                                                                    tuberosum cDNA
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536
                                   837 caccaagaaaatacagacttgtacaataag 866
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                                                                                                         aagaaggaccatctcttgatagatgagattcacgatttgaatcgaaaggcaagtttattt 836
                                                                                                                                                                                                                                                                                                                                                                                                                                                      accagcatgaaatcagttatagatcggtacggcaaggccaaggaagagcagcaagtcgtc 596
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gatgoggaggtoggcotogtoatottotocagcacoggcogcototacgagtactotagc 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           tcgatggggaggggaaagatcgtgatccgcaggatcgataactccacgagccggcaggtg 416
CATCAAGAAATTTGGAACTCTACAAGAAG
                                                                                AAAAAGGAGCAAATATTGAAGGATGAAATTCAAGAGCTAACTCGAAAGGGGAGCATAATA 535
                                                                                                                                                                    GTAAAAGAACTAACAGATCTGGAGAATCAACTGGAAATGAGCTTAAAGGGAATCCGTATG 475
                                                                                                                                                                                          gtcaaagaactgcagtccctggagaatcaattggaaacaagcctgcgtggtgtccgcgca 776
                                                                                                                                                                                                                                                       CTACAGGATCTGCAAGGGAATCAACGGCAATTATTGGGAGAGGAGGTAAGTGGTTTGGGC 415
                                                                                                                                                                                                                                                                                             ctgcacaacttgcaagaaaattatcggcagttgacgggagatgatctttctgggctgaat 716
                                                                                                                                                                                                                                                                                                                                        gcaaatcccaactcggagcttaagttttggcaaagggaggcagcaagcttgagacaacaa 656
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACTTTCTCAAAGAGAAGGAATGGATTGTTGAAGAAAGCTAAGGAGCTCGCGATTCTTTGC 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          accttctccaagcgccggaacgggatcttcaagaaggccaaggagctcgccatcctctgc 476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TAGATGGGAAGGGGAAAGATAGTGATCCGAAGGATCGATAACTCAACGAACAGGCAAGTT 115
                                                                                                                                                                                                                                                                                                                                                                                                                               ACCAGCATGAAATCAGTTATTGAACGATACACCAAAACGAAGGACGATTGTCAGCAATTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GATGCTGAAGTTGGATTGATTATTTTCTCTAGTACTGGAAAGCTCTATGAGTTTTCTAAC 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          356;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Research Genetics, Libraries Division Tel: 1-800-711-6195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        For clone info: please contact Research Genetics, Division tel_1-800-711-6195, email cdna@resgen.co
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Asteridae; euasterids I;
1 (bases 1 to 716)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: cdna@resgen.com
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Generation of ESTs from potato roots
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tanksley, S. and Baker, B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Utterback, T., Chiemingo, A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     van der Hoeven, R., Sun, H., Karamycheva, S.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 inote="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2: XhoI; supplier: Cornell University, Tanksley lab; sequencing; The Institute for Genomic Research. Roots wei isolated from in vitro grown stem cuttings on CM medium. Roots were isolated two weeks after placing the stem cuttings from in vitro grown plants on medium."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone_lib="potato roots"
/tissue_type="roots"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /lab_host="SOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /dev_stage="in vitro grown stem cuttings"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /db_xref="taxon:4113"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Solanum tuberosum"
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Pred, No. 1.8e-33;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cdna@resgen.com
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 10;
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mes 322; Conserv
                                                                                                                                                                                    caaatcccaactcggagcttaagttttggcaaagggaggcagcaagcttgagacaacaac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 atgcggaggtcggcctcgtcatcttctccagcaccggccgcctctacgagtactctagca 537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ccttctccaagcgccggaacgggatcttcaagaaggccaaggagctcgccatcctctgcg 477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CGATGGGGAGAGGTAAGATAGTGATAAGGAGGATCGATAATTCGACGAGCAGCCAGGCAAGTGA 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cgatggggaggggaaagatcgtgatccgcaggatcgataactccacgagccggcaggtga 417
                                                                                                                                                                                                                                                                                                                                                          ccagcatgaaatcagttatagatcggtacggcaaggccaaggaagagcagcaagtcgtcg 597
                                                                                                                                                                                                                                                                                                                                                                                                                                       ATGCGGAGGCCGGAGTTATTATCTTCTCCAGTACTGGAAAACTCTATGAATATTCAAACA 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CGTTCTCGAAGAGGAGAAATGGATTGCTGAAGAAGGCGAAGGAGCTAGCGATTCTGTGCG
   TTCAGAACTTGCAAGAGAATCACCGACAAATGATGGGTGAGGAACTTTCTGGTCTGAGCG
                                                             tgcacaacttgcaagaaaattatcggcagttgacgggagatgatctttctgggctgaatg 717
                                                                                                                                              AAACTCCAACTTCTGAGGTTAGGTTTTGGCAAAGGGAAGCGGCAATGCTGAGGCAACAAC
                                                                                                                                                                                                                                                                                                CCAGCATGAAGTCTGTGATTGAAAGATACAACAGAACAAAGGAGGAGAATCATCAATTGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
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/tisue_type="radicle"
/dev_stage="seedlings 5 days post-imbibition"
/dev_stage="seedlings 5 ft".); Site_1: EcoR1; Site_2:
/note="Vector: pBlueScript SK(-); Site_1: EcoR1; Site_2:
/note="seedlings ft".]; Site_1: EcoR1; Site_2: EcoR1; Site_2
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University"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Lycopersicon
/cultivar="TA496"
/db_xref="taxon:4081"
/clone="cLEZ6G19"
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73.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 253; DB 9;
Pred. No. 9.5e-32;
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caaatcccaactcggagcttaagttttggcaaagggaggcagcaagcttgagacaacaac 657
                                                                                           atgeggaggteggeetegteatetteteeageaceggeegeetetaegagtaetetagea 537
                                                                                                                                                                                                     CGTTCTCGAAGCGAAGAAATGGATTGCTCAAGAAAGCCAAGGAGCTTGGCATCCTTTGTG
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                                                                   CCAGCATGAAGTCTGTAATTGACCGTTATAATAAAACAAAAGAGGAGCAAAGTCAGTTGG
                                                                                                                                                                                                                                                                                                                                           367;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 (bases 1 to 812)
Bohnert, H.J., Borchert, C., Brazille, S., Brooks, J., H., Kawasaki, S., McCollough, A., Michalowski, C.B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       mads-box protein agll7-like protein, mRNA sequence {\tt BE034403}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BE034403 MH Mesembryanthemum crystallinum cDNA 5' similar
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  University of Arizona
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Michalowski, C.B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         common ice plant.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: cbm@u.arizona.edu
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520-621-1697
                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="grown in hydroponics,
Hoagland's), 78 h stress"
176 c 168 g 193 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Mesembryanthemum crystallinum"
/db_xref="taxon:3544"
/clone_lib="MH"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /tissue_type="roots"
/dev_stage="5-6 weeks"
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CGTTCTCGAAGAGGAGAAATGGATTGTTGAAGAAGGCCAAGGAGCTAGCGATTCTGTGCG
                  cettetecaagegeceggaaegggatetteaagaaggceaaggagetegeeateetetgeg 477
                                                                          CGATGGGGAGAGGAAAGATAGTGATAAGGAGGATCGATAATTCGACGAGCAGGCAAGTGA 204
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                                                                                                                                                        307;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           van der Hoeven,R., Bezzerides,J., Sun,H., Cho,J., Chieminge Bougri,O., Buell,C.R., Ronning,C., Tanksley,S. and Baker,B. Generations of ESTs from sprouting potato eyes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Cathy Ronning
The Institute for Genomic Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    potato.
Solanum tuberosum
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BG592879.1 GI:13611019
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   For clone info: please contact Division tel 1-800-711-6195, em
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Asteridae; euasterids I; Solanales; Solanaceae; Solanum 1 (bases 1 to 553)
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                                                                                                                                                                                                                                                                         163
                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                     taken from tubers. The tubers were incubated at 26C in the dark for 2-3 weeks prior to sprouting. The eyes were frozen in liquid nitrogen immediately upon removal from tubers."
                                                                                                                                                                                                                                                                                                                                                         /note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2: XhoI; Various sizes of sprouting eyes (Jmm to 15mm) were
                                                                                                                                                                                                                                                                                                                                                                                                        /lab_host="SOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                        /tissue_type="sprouting
/dev_stage="12-14 weeks
                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone_lib="cSTS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone="cSTS2N7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /db_xref="taxon:4113"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Solanum tuberosum"
/cultivar="Kennebec"
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75.1%;
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                                                                                                                                                      Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: kate@mail.bio.tamu.edu of ther name: 25·C·1; date: 7/6/99; Submitted to the Database of Expressed Sequence Tags (dbEST) on 08/25/99; More information available at 'http://chrysie.tamu.edu/medicago'. Seq primer: SKmod (CTA gAA CTA gTg gAT CC).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Texas A&M University
College Station, TX 77843-3258,
Tel: 409 845 7707
Fax: 409 845 2891
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AI974336
AI974336.1 GI:5776633
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished (1999)
Contact: VandenBosch K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae
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                     152
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                     ۵
                                     /note-"vector: pBluescript SK -; Site_1: EcoRI; Site_2: XhOI; cDNA was prepared from polyA+ enriched RNA. The cDNA was directionally ligated into the Unizap XR vector from Stratagene and packaged using Gigapack III Gold packaging extracts. Plasmids containing cDNA inserts were excised from the recombinant lambda-Zap phage using Ex-assist helper phage and propagated in XLOLR cells."
                                                                                                                                                                                                                    /tissue_type="Seedling roots"
/dev_stage="Immediately prior to inoculation with
Sinorhizoblum meliloti (0 hour)"
                helper phage and propagated in 77 c 131 g 127 t
                                                                                                                                                                                                                                                                                        /clone_lib="KV0"
                                                                                                                                                                                                                                                                                                                                                      /organism="Medicago truncatula"
/cultivar="genotype_A17"
                                                                                                                                                                                               /lab_host="E.coli strain XLOLR"
                                                                                                                                                                                                                                                                                                                  /clone="pKV0-1J1"
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                                                                                                                                                                                                                             Sequences have been trimmed to exclude PolyA, vector, and regions below Phred quality 16. The threshold for highest quality sequence is 20. Three-prime sequences, which are obtained with PolyTMix or
                                                                                                                                                                                                                                                                                                                                      The University of Georgia Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cordonnier-Pratt,M.-M., Gingle,A., Fang,G.C., Dean,R., Wing,R., Sudman,M. and Pratt,L.H.
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Sorghum bicolor
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                                                                                                                                                                                            Seq primer: JEN REV
                                                                                                                                                                                                                                                                                         Email: mmpratt@uga.edu
                                                                                                                                                                                                                                                                                                                                                                                      Department of Botany
                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Cordonnier-Pratt MM
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                                                                                                                                                                                                                                                                                                                                                                                                                                             pathogen
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706 542 1805
                                                                                                                                                                        quality sequence stop: 470
/clone_lib="Pathogen-infected compatible 1 (PIC1)"
/tissue_type="Leaves"
/dev_stage="4-week-old seedlings infected with
                                                         /organism="Sorghum bicolor"
/cultivar="BTx623"
/db_xref="taxon:4558"
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354 agatcgatggggaaggggaaagatcgtgatccgcaggatcgataactccacgagccggcag 413
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CAACTGCACAACTTGCAAGAGGAGCCACAAGCAACTAATGGGAGAGGA 499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gtcgcaaatcccaactcggagcttaagttttggcaaagggaggcagcaagcttgagacaa 653
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TGCGATGCGGAGGTTGGCCTCATCATCTTCTCCAGCACCGGAAGGCTCTACGAGTTCTCC
The University of Georgia
Plant Sciences Building, Rm.
Tel: 706 542 1805
Fax: 706 542 1805
                                                                                                                                                                                                                                                                                                                        Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Sorghum.

1 (bases 1 to 581)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sorghum bicolor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sorghum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BE596704
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PI1_58_F04.b1_A002 Pathogen induced 1 (PI1) Sorghum bicolor cDNA,
                                                                                                                          Department of Botany
                                                                                                                                                               Contact: Cordonnier-Pratt
                                                                                                                                                                                          Unpublished (2000)
                                                                                                                                                                                                                            An EST database from Sorghum:
                                                                                                                                                                                                                                                                                             Cordonnier-Pratt, M.-M., Gingle, A., Dean, R., Sudman, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BE596704.1 GI:9851777
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Colletotrichum graminicola"
/note="Vector: pBluescript II SK(-) from Lambda Zap Site_1: XhoI; Site_2: EcoRI; Four-week-old sorghum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18.5%;
80.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            581 bp
                                                             2502, Athens, GA 30602-7271, USA
                                                                                                                                                                                                                                pathogen-induced plants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            mRNA
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RESULT 1
AL389596
                                                 SOURCE
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                                                                                                                                                           DEFINITION
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                414
                                                                                                                                                                                                                                                                                      391 CAACTGCACAACTTGCAAGAAA 412
                                                                                                                                                                                                                                                                                                                                                                          331 ACCAACAATGCAACTTCAGAACTCATGCTCTGGCAAAGGGAGGCAGCAAGCTTGAGGCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                               271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     534 agcaccagcatgaaatcagttatagatcggtacggcaaggccaaggcaaggagcagcaagtc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    474 tgcgatgcggaggtcggcctcgtcatcttctccagcaccggccgcctctacgagtactct
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    caactgcacaacttgcaagaaa 675
                                                                                                                                                                                                                                                                                                                                                                                              gtcgcaaatcccaactcggagcttaagtttttggcaaagggaggcagcaagcttgagacaa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GTGACCTTCTCTAAGAGACGGAACGGGCTGCTGAAGAAGGCAAAGGAGCTCTCAATCCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gtgaccttctccaagcgccggaacgggatcttcaagaaggccaaggagctcgccatcctc 473
                                                                                                                                                                                                                                                                                                                                                                                                                                                             AGCACCAACATGAAAGCTGTGATAGACCGATACGGAAAGGCAAAAGAGGAGCAGATTGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TGCGATGCGGAGGTTGGCCTCATCATCTTCTCCAGCACCGGAAGGCTCTACGAGTTCTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              265;
                                                                     EST
                                                                                                                                                      MtBC56A01F1 MtBC Medicago
      Eukaryota;
                        Medicago truncatula
                                                                                            AL389596.1
                                                                                                              AL389596
                                                                                                                                    sequence.
                                                                                                                                                                               AL389596
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Seq primer: JEN REV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequences have been trimmed to exclude PolyA, vector and regions below Phred quality 16. The threshold for highest quality sequence
                                                 barrel medic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             High quality sequence stop: 497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: mmpratt@uga.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cultivar) were infected with pathogen (isolate FRM42I of Colletotrichum graminicola, which is a sorghum isolate). RNA was prepared from infected leaves harvested from 45 seedlings 48 hours after inoculation. Note: young
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     two-week-old sorghum plants 48 hr after inoculation;
Vector: pBluescript II from Lambda Zap II; Site_1: X
Site_2: EcoRI; Two-week-old sorghum plants (BTX 623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RNA in the cloning vector lambda ZAP II. Clones to be sequenced were prepared by mass excision. WARNING: While most or all ESTs are expected to derive from the host
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 grow older (4 weeks or older), plants resume susceptiblity to anthracnose disease. The library was made from poly-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            seedlings (2 weeks old) exhibit juvenile resistant reaction, which is an incompatible interaction. As they
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              plant, no effort was made to eliminate ESTs deriving from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone_lib="Pathogen induced 1 (PI1)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Sorghum bicolor"
/db_xref="taxon:4558"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="Organ: Anthracnose-infected leaves from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                                                                                            GI:9689347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     pathogen.
120 c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 230.8; DB IU;
Pred. No. 3.9e-28;
""" matches 57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     141 g
                                                                                                                                                                             492 bp
                                                                                                                                                      truncatula cDNA clone MtBC56A01
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 10; Length 581;
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DЬ Qy В Qy В Qγ Вþ Qy Дb Qy Ър QΥ

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303
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                         592 tcgtcgcaaatcccaactcggagcttaagttttggcaaagggaggcagcaagcttgagac 651
                                                                                                                                                                                                                                                                            472 totgogatgoggaggtoggoctogtoatottotocagoacoggoogoctotacgagtact 531
                                                                                                                                                                                                                                                                                                                                                                  123 AAGTAACTTTTTCGAAGCGAAGGAATGGATTGTTGAAGAAGGCGAAGGAACTTGCGATTT 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       353 gagatcgatggggagggaaagatcgtgat-ccgcaggatcgataactccacgagccggc 411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       63 GATAGAAATGGGGAGAGGAAAGATCCAGATGAAGGAGGATTGATAATTCGACGAGCAGGC 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local
                                                                                                                                                    aggtgaccttctccaagcgccggaacgggatcttcaagaaggccaaggagctcgccatcc 471
AACTTGGGAGTTCAACCTCTGAAATTAAGTTTTGGCAAAAGGGAGGCAGCAATGTTAAGGC
                                                                                                                                                                                                                                      TGTGCGATGCTGAGGTTGGGGTTATGATCTTCTCCAGCACTGCAAAACTCTATGATTTCG 242
                                                                                                                 CCAGCACCAGCATGAGATCAGTAATTGATCGGTACAACAAAACTAAAGAAGAACACAATC 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         309;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact : Pascal Gamas and Etienne-Pascal Journet, Laboratoire Biologie Moleculaire des Relations Plantes-Microorganismes,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             http://sequence.toulouse.inra.fr/Mtruncatula.html)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CNRS-INRA, BP 27 31326 Castanet-Tolosan Cedex, France (Email:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BP 191 91006 EVRY cedex - France
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished (2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Journet, E.P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: segref@genoscope.cns.fr,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                , V. and Gamas, P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (bases 1 to 492)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      into Uni-zap XR vector from Stratagene and packaged using Gigapack Gold packaging extracts. Plasmids containing cDNA inserts were mass-excised from phage stocks using ExAssit helper phage and propagated in SOLR cells. Clone ordering
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              XhoI; M. truncatula sterilised seeds were germinated for 72h at 25 C, before transplanting into a 1/3 Epoisses soil 2/3 calcined Terragreen mix in the presence of onion root fragments colonized by the arbuscular mycorrhizal fungus Glomus intraradices (Schenck & Smith, isolate LPA8). The plants were watered every day and twice a week with a modified nutrient Long Ashton solution without phosphate but with a high level of nitrate. After 3 weeks RNA was extracted from whole root systems. CDNA was prepared from polyA+ enriched RNA. The CDNA was directionally ligated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   and sequencing was performed by the Centre National de
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This clone is available through: ResGen, Invitrogen Corp. South Memorial Parkway Huntsville, AL 35801 For further in call: (800)-533-4363 or contact via email: ccu@resgen.com
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tel: 314 286 1800 Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Shoemaker R/Public Soybean EST Project Public Soybean EST Project Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, Tel: 314 286 1800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Shoemaker.R., Kelm.P., Vodkin,L., Erpelding,J., Coryell,V., Khanno,A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C. Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schur,R., Ritter,B., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and Wilson,R.
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Glycine max
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       est@watson.wustl.edu
            þ
                                                                   pSuperScript cDNA library construction kit. Complimentary DNA was synthesized from mRNA using a poly (dT) sequence with a Not I restrictions site. Sal I linkers adapers were ligated to the blunt-ended cDNA fragments followed by Not I digestion. The cDNA fragments were directionally cloned into the Not I Sal I restriction site of the psport vector. The ligated cDNA fragments were transformed into E.coli Electromax DH10B host cells. This
                                                                                                                                                                                                                                                                   cDNA library was constructed from mRNA isolated from seed coats (100-200mgs) of greenhouse grown plants. The library was prepared using the Life Technologies
                            library was constructed by {\tt Dr.\ Lila\ Vodkin\ and\ Dr.\ Anu\ Khanna."}
                                    Khanna
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                                                                                                                                                                           Contact: Olin Anderson
US Department of Agriculture, Agriculture Research
West Area, Western Regional Research Center
800 Buchanan Street, Albany, CA 94710, USA
                                                                                                                                                                                                                                                                                                                                   Anderson,O.D., Chao,S., Choi,D.W., Close,T.J., Fenton,R.D., Han Anderson,O.D., Kang,Y., Lazo,G.R., Miller,R., Nguyen,H.T., Rausch,C.J., Seaton,C.L., Tong,J.C. and Zhang,D.

The structure and function of the expressed portion of the wheat
                                         quality sequence with phred score less than Seq primer: Stratagene SK primer.
                                                                Sequence have been trimmed to remove vector sequence quality sequence with phred score less than 20
                                                                                                                                                                   800 Buchanan Street,
Tel: 5105595773
                                                                                                                                                                                                                                                                                          genomes - Normalized root cDNA library Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae; Triticeae; Triticem.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BE445262 587 bp mRNA linear EST 25-WHE1133_A05_A09ZS Wheat etiolated seedling root normalized library Triticum aestivum cDNA clone WHE1133_A05_A09, mRNA
                                                                                                                                              Fax: 5105595818
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Triticum aestivum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          bread wheat.
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                                                                                                                  oandersn@pw.usda.gov
                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GI:9444818
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16.7%;
65.9%;
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                                                                                                                                                                                                                                           Service, Pacific
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EST 25-JUL-2000

429

309

CDNA

low

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BASE COUNT
Search completed: August 11, 2002, 08:05:38 Job time: 8322 sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            349
                                                                                                                                                                                                                                                                                                                      656 actgcacaacttgcaagaaaattatcggcagttgacgggagatgatctttctgggctgaa 715
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      479 tgcggaggtcggcctcgtcatcttctccagcaccggccgcctctacgagtactctagcac 538
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        169 GATGGGGAGGGGAAGATTGCGATTGAGAGGATCGACAACGCGACGAACCGTCAGGTGAC 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 359 gatggggaggggaaagatcgtgatccgcaggatcgataactccacgagccggcaggtgac 418
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   229 CTTCTCCAAGCGGCGCGGAGGGCTGATGAAGAAGGCCCGGGAGCTCGCCATCCTCTGCGA 288
                                                                                                                                                                                                                  716 tgtcaaagaactgcagtccctggagaatcaattggaaacaagcctgcgtggtgtccg 772
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cagc---atgaaatcagttatagatcggtacggcaaggccaaggcaagagcagcaagtcgt 595
                                                                                                                                                             AGTGCAGAACTTACAACACAATAATAGGCAACTATTGGGAGAGGAACTATCTGGTTCCAC 528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CAGCGGAATGGAGGCAATACTAGAGCGCTACCAGGAGGCCAAACAGGAGCATTGTGGAGT 408
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               excised to give pBluescript phagemids before normalization was carried out. The mass excision of phagemid library and normalization were done in HT Nguyen lab by D. Zhang at Texas Tech University. Normalization protocol used was that of Soares. Plasmid DNA preparations and DNA sequencing were performed in the OD Anderson lab (all other authors)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note-"Vector: Lambda Uni-ZAP XR, excised phagemid pBluescript SK; Site_1: EcoRI; Site_2: XhoI; Seeds were surface-sterilized, germinated and grown asseptically in the dark at room temperature on filter paper with water, nystatin and cefotaxime in covered crystallization dishes. Roots were harvested. The tissue, total RNA, and poly(A) RNA were prepared, a cDNA library was made in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Triticum aestivum"
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/db_xref="taxon:4565"
/clone="WHE1133_A05_A09"
/clone=_lib="Wheat etiolated seedling root normalized cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     poly(A) RNA were prepared, a cDNA library was made in t TJ Close lab (Choi, Close, Fenton) at the University of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         library"
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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     Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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US-09-460-512-4
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US-08-655-227-6
US-08-655-227-8
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235.427 Million cell updates/sec
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381	382.5	382.5	382.5	382.5	382.5	382.5	383	383	383	383	383.5	383.5	383.5	383.5	385	385	385
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US-08-867-087B-2	US-09-398-326-10	US-09-149-976-10	US-08-655-241-10	US-08-655-227-10	US-08-659-188-10	US-08-592-214A-10	US-09-398-326-2	US-08-655-241-2	US-08-655-227-2	US-08-659-188-2	US-09-149-976-2	US-08-592-214A-2	US-08-576-156-2	US-08-867-087B-55	US-09-398-326-8	US-09-149-976-8	US-08-655-241-8
Sequence 2, Ap	Sequence 10, A	Sequence 10, A	Sequence 10, A	•	•	•	Sequence 2, Ap	Sequence 2, Ap	Sequence 2, Ap	-	Sequence 2, Ap	Sequence 2, Appl	Sequence 2, Appl	Sequence 55, A	Sequence 8, Appli	Sequence 8, Appl	Sequence 8, Appli
Appli	ppl	Tdd	Appl	Appl	Appl	Appl	Appli	Appli	Appli	Appli	Appli	pli	pli	Appl	ild	1 Td	pli

## ALIGNMENTS

RESULT 1 US-08-460-512-5

; Sequence 5, Application US/08460512
; Patent No. 5744693

GENERAL INFORMATION:
APPLICANT: MEYEROWITZ, Elliot

APPLICANT:

YANOFSKY, Martin F.

3

PLANTS HAVING ALTERED FLORAL DEVELOPMENT

APPLICANT: MA, Hong

CORRESPONDENCE ADDRESS: TITLE OF INVENTION: NUMBER OF SEQUENCES:

ADDRESSEE:

Richard F.

Trecartin

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; MOLECULE TYPE: US-08-460-512-5
Query Match
Best Local Similarity
                                                                                                                                                       TELEFAX: (415) 398-324
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 252 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/460,512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                  REGISTRATION NUMBER: 31,801
REFERENCE/DOCKET NUMBER: A-57322/RFT
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION: NAME: Trecartin, Richard
                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 800 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 4 Embarcadero Center, Suite 3400 CITY: San Francisco
                                                                                                        TYPE: amino acid
STRANDEDNESS: sir
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP:
                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                              FILING DATE: APPLICATION NUMBER: US/07/956,694
                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/293,278
                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
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                                                                                                                                                             252 amino acids
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                                                                                         peptide
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                                                                                                                                                                                                                  398-3249
                                                                                                                                                                                                                                                                                                         Richard F
 35.1%;
41.1%;
   Score 426.5; DB 1;
Pred. No. 6.6e-33;
                  Length 252;
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; MOLECULE TYPE: US-08-460-512-2
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US-08-460-512-2
   Matches
                   Best
                                Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: MEYEROWILL, APPLICANT: YANOFSKY, Martin F.
APPLICANT: MA, Hong
APPLICANT: MA, HONG
APPLICANT: MA, HONG
APPLICANT: MA, HONG
                                                                                                                                                        SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION: TELEPHONE: (415) 781-1989
                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 800 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
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CITY: S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     192 RNNPSISLMPGGSNYEQLMPPP-----QTQSQPFDSRNYFQVAAL-QPNNHHYSSAGRQ 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  179 ELHKKIYETEGPSGVNRESPTPFNFAVVETRDVPVQ----LELSTLPQQNNIEPSTA---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 136 SPKELRNLEGRLERSITRIRSKKNELLFSEIDYMQKREVDLHNDNQILRAKI----AENE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            119 NVKELQSLENQLETSLRGVRAKKDHLLIDEIHDLNRKASLFHQENTDLYNKINLIRQEND 178
                Local Similarity
                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: A-
                                                                                                           TOPOLOGY:
                                                                                                                            TYPE:
                                                                                                                                                                                                   TELEPHONE:
                                                                                                                                                                                                                                                NAME: Trecartin, Richard F
REGISTRATION NUMBER: 31,80
                                                                                                                                                                                                                                                                                                              FILING DATE: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER:
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                                                                                                                                        LENGTH:
                                                                                                                                                                                                                                                                                                FILING DATE
                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      102;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MKSVIDRYGKAKEEQQ----VVANPNSELKFWQREAASLRQQLHNLQENYRQLTGDDLSGL 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       102;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        E: Richard F. Trecartin
4 Embarcadero Center, Suite 3400
                                                                                                                                        285 amino acids
   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                     PatentIn Release #1.0, Version #1.25
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                                                                                                           linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Floppy disk
            35.1%; Score 426.5; DB 1 41.1%; Pred. No. 7.9e-33;
                                                                                                                                                                                                                                                                                                              US/07/956,694
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   49;
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                                                                                                                                                                                                                                   A-57322/RFT
   Mismatches
                           DB 1;
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                           Length 285;
Indels
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23;
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7;
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                                                                                      ; MOLECULE TYPE: US-08-460-512-4
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                         Query Match
Best Local Similarity
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            Matches 104;
                                                                                                                                                                                TELEFAX: (415) 398-32 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: A-TELECOMMUNICATION INFORMATION: TELEPHONE: (415) 781-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
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                                                                                                                    TOPOLOGY:
                                                                                                                                    TYPE:
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                                                                                                                                                 LENGTH:
                                                                                                                                                                                                                                                              REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              OPERATING SYSTEM:
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            Conservative
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                                                                                                                 linear
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SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        119 NVKELQSLENQLETSLRGVRAKKDHLLIDEIHDLNRKASLFHQENTDLYNKINLIRQEND 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       111 VKGTIERYKKAISDNSNTGSVAEINAQ--YYQQESAKLRQQIISIQNSNRQLMGETIGSM 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  51 GRGKIEIKRIENTTNRQVTFCKRRNGLLKKAYELSVLCDAEVALIVFSSRGRLYEYSNNS 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GRGKIVIRRIDNSTSRQVTFSKRRNGIFKKAKELAILCDAEVGLVIFSSTGRLYEYSSTS 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ELHKKIYETEGPSGVNRESPTPFNFAVVETRDVPVQ----LELSTLPQQNNIEPSTA--- 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RNNPSISLMPGGSNYEQLMPPP-----QTQSQPFDSRNYFQVAAL-QPNNHHYSSAGRQ 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Application US/08460512
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  YANOFSKY, Martin F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            E: Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Richard F. Trecartin
                      34.4%; Score 418.5; DB 1 40.0%; Pred. No. 3.8e-32;
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    Mismatches
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MOLECULE TYPE: protein
US-09-067-800-8
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                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                         Query Match
Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       179 ELHKKIYETEG-----PSGVNRE-----SPTPFNFAVVETRDVPVQLELSTLPQ 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        119 NVKELQSLENQLETSLRGVRAKKDHLLIDETHDLNRKASLFHQENTDLYNKINLTRQEND 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                233 PNNHHYSSAGREDQTALQLV 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          223 QNNIEPSTA---PKLGLQLI 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             182 LLRAKIAENERNNPSMSLMPGGSNYEQIMPPPQTQPQPF-----DSRNYFQVAAL-Q 232
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CLASSIFICATION:
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OPERATING SYSTEM: PC-DOS/MS-DOS
COMPUTATION OF THE PC-DOS 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Campbell, Cathryn A. REGISTRATION NUMBER: 31,815
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: San Diego
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                                       61 SMKSVIDRYGKAKEEQQVVANP----NSELKFWQREAASLRQQLHNLQENYRQLTGDDLS 116
                                                                                                                 16
                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: P-UD 2948
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/09/067,800
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                                                                                                                                                                                    1 MGRGKIVIRRIDNSTSROVTFSKRRNGIFKKAKELAILCDAEVGLVIFSSTGRLYEYSST 60
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                                                                                                                 IGRGKIEIKRIENTTNRQVTFCKRRNGLLKKAYELSVLCDAEVALVIFSTRGRLYEYANN 75
                                                                                                                                                                                                                                                                  96;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       246 amino acids
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                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Campbell & Flores LLP
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                                                                                                                                                                                                                                                                                                 34.3%;
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                                                                                                                                                                                                                                                                  53;
                                                                                                                                                                                                                                                                                                 Score 417; DB 4; Length 246; Pred. No. 5.1e-32;
                                                                                                                                                                                                                                                                  Mismatches
73;
                                                                                                                                                                                                                                                                  Indels
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                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (619) 535-8949 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
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APPLICANT: Ferrandiz, Cristina
TITLE OF INVENTION: Seed Plants Characterized by Delayed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION: (619) 535-9001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      232 PKLGLQLI 239
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117 GLNVKELQSLENQLETSLRGVRAKKDHLLIDEIHDLNRKASLFHQENTDLYNKI----NL 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET:
CITY: S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   76 SVRGTIERYKKACSD---AVNPPTITEANTQYYQQEASKLRRQIRDIQNLNRHILGESLG 132
                                           76
                                                                                                                           16
                                                                                                                                                                                                            7 Match 34.3%; Score 417; DB 4; Length 246; Local Similarity 38.7%; Pred. No. 5.le-32; nes 96; Conservative 53; Mismatches 73; Indels
                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Campbell, Cathryn A REGISTRATION NUMBER: 31,8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                               TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: P-UD 2948
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                                                                                                                                                                                                                                                                                                                                                                                                LENGTH:
                                                                                                                                                                1 MGRGKIVIRRIDNSTSRQVTFSKRRNGIFKKAKELAILCDAEVGLVIFSSTGRLYEYSST 60
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                                                                                                                         SVRGTIERYKKACSD---AVNPPTITEANTQYYQQEASKLRRQIRDIQNLNRHILGESLG 132
                                                                                  SMKSVIDRYGKAKEEQQVVANP----NSELKFWQREAASLRQQLHNLQENYRQLTGDDLS 116
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                                                                                                                                                                  Matches
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                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                               TELEFAX: (415) 398-32 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL
                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: A-57322/RET TELECOMMUNICATION INFORMATION: TELEPHONE: (415) 781-1980
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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          120 VKELQSLENQLETSLRGVRAKKDHLLIDEIHDLNRKASLFHQENTDLYNKINLIRQENDE 179
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                                                                                                        17
                                                           CITY: San Francisco
STATE: California
                                                                                                                                                                               Local Similarity
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                                                                                                                                                                                                                                                                                                LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/07/956,694
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER:
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                                                                                                                     SVKATIERYKKACSDSSNTGSISEANAQYYQQEASKLRAQIGNLQNQNRNMLGESLAALS 136
                                                                                                    LGRGKIEIKRIENTTNRQVTFCKRRNGLLKKAYELSVLCDAEVALIVFSSRGRLYEYANN 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QQQESSVIHQGTVYES-GVTSSHQSGQYNRNYIAVNLLE------PNQNSSNQDQP 241
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                                                                                                                                                                                                                                                                                   : 248 amino acids amino acid
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                                                                                                                                                                 Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                      protein
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                                                                                                                                                            Score 409.5; DB 1;
Pred. No. 2.7e-31;
51; Mismatches 72;
                                                                                                                                                                                          Length 248;
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                                                                                                                                                                                                                                                                                                                  Query Match
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                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE:
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TELECOMMUNICATION INFORMATION:
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 193
                                   171
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OTTY: San Diego

OTTY: Thirder
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                226 IEPSTAPKLGL 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 183 LRAKIAETERAQQQQQQQQMNLMPGSSSYELVPPPHQF---DTRN----YLQVNGLQTNNH 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   180 LHKKIYETEGPSGVNRES-------PTPFNFAVVETRDVPVQLELSTLPQQNN 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      137 LRDLKNLEQKIEKGISKIRSKKNELLFAEIEYMQKR-----EIDLHN-----NNQY 182
                                                                                                                                                                                                                                                                                 Local Similarity 43.9 nes 90; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0
                                                                                                                                            76
                                                                                                                                                                             61
                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Campbell, Cathryn A. REGISTRATION NUMBER: 31,815
                                                                                                                                                                                                             16 LGRGKIEIKRIENTTNRQVTFCKRRNGLLKKAYELSVLCDAEVALVIFSTRGRLYEYANN 75
                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: United States ZIP: 92122
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                                                                                                                                                                                                                               GLNVKELQSLENQLETSLRGVRAKKDHLLIDEIHDLNRKASLFHQENTDLYNKI-----
NPDQQESSVIQGTTVYE----SGVS
                                   NLTRQENDELH-KKIYETEGPSGVN 194
                                                                      SLNFKELKNLEGRLEKGISRVRSKKNELLVAEIEYMQKREMELQHNNMYLRAKIAEGARL 192
                                                                                                                                          SVRGTIERYKKACSD---AVNPPSVTEANTQYYQQEASKLRRQIRDIQNSNRHIVGESLG 132
                                                                                                                                                                           SMKSVIDRYGKAKEEQQVVANPNS----ELKFWQREAASLRQQLHNLQENYRQLTGDDLS 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         California
                                                                                                                                                                                                                                                                                                                                                                                                                                              248 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4370 La Jolla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (619) 535-8949
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ferrandiz,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Yanofsky, Martin F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Campbell & Flores LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (619) 535-9001
                                                                                                                                                                                                                                                                                                                                                                                           protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Floppy disk
                                                                                                                                                                                                                                                                               33.3%; Score 405; DB 4; L
43.9%; Pred. No. 7.2e-31;
43.9%; Mismatches 55;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Seed Dispersal
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213
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                                                                                US-08-867-087B-17
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                      Sequence 17, Application US/08867087B Patent No. 5990386 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 33.3%; Score 405; DB 4; Length 248; Best Local Similarity 43.9%; Pred. No. 7.2e-31; Matches 90; Conservative 42; Mismatches 55; Indels
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APPLICANT: Ferrandiz, Cristina
APPLICANT: Seed Plants Characterized by Delayed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
           APPLICANT:
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                                                                                                                                                      193 NPDQQESSVIQGTTVYE----SGVS 213
                                                                                                                                                                                     171 NLIRQENDELH-KKIYETEGPSGVN 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE: C
                                                                                                                                                                                                                                                           117 GLNVKELQSLENQLETSLRGVRAKKDHLLIDEIHDLNRKASLFHQENTDLYNKI-----
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                      16 LGRGKIEIKRIENTTNRQVTFCKRRNGLLKKAYELSVLCDAEVALVIFSTRGRLYEYANN 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE:
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                                                                                                                                                                                                                                                                                                                                                                                       LENGTH:
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                                                                                                                                                                                                                                                                                                                              SMKSVIDRYGKAKEEQQVVANPNS----ELKFWQREAASLRQQLHNLQENYRQLTGDDLS 116
                                                                                                                                                                                                                       SINFKELKNIEGRIEKGISRVRSKKNELLVAEIEYMQKREMELQHNNMYLRAKIAEGARL 192
                                                                                                                                                                                                                                                                                              SVRGTIERYKKACSD---AVNPPSVTEANTQYYQQEASKLRRQIRDIQNSNRHIVGESLG 132
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4370 La Jolla Village Dr
         An, Gynheung
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                                                                                                                                                                                                                                                                                                                                                                                                                                              18;
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; Sequence 4, Application US/08592214A
; Patent No. 5811356
; GENERAL INFORMATION:
; APPLICANT: Yanofsky, Martin F.
                                                                      RESULT 10
US-08-592-214A-4
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US-08-867-087B-17
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (503) 228-9446 INFORMATION FOR SEQ ID NO: :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION: TELEPHONE: (503) 226-7391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 800
PRIOR APPLICATION NUMBER: U.S. 08/323,449
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CORRESPONDENCE ADDRESS:
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                                                                                                                                                                    113 NLLGEDIGTIGIKELEQLEKQLDSSLRHIRSTRTQHMLDQLTDLQRREQMLCEANKCLRR 172
228 GFTPEQMNNSCVTA 241
                                      218 STLPQQNNIEPSTA 231
                                                                                                                          169 KINLIRQENDELHKKI------YETEGPSGVNRESPTPFN--FAVVETRDVPVQLEL 217
                                                                                                                                                                                                           109 QLTGDDLSGLNVKELQSLENQLETSLRGVRAKKDHLLIDEIHDLNRKASLFHQENTDLYN 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Klarquist Sparkman Campbell Leigh ADDRESSEE: Whinston, LLP STREET: One World Trade Center STREET: 121 S.W. Salmon Street STREET: Suite 1600 CITY: Portland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: October 14, 1994
APPLICATION NUMBER: U.S. 08/485,981
FILING DATE: June 7, 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: UZIP: 97204
                                                                                                                                                                                                                                                                                                 60 TSMKSVIDRYGK------AKEEQQVVANPNSELKFWQREAASLRQQLHNLQENYR 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                       1 MGRGKIVIRRIDNSTSRQVTFSKRRNGIFKKAKELAILCDAEVGLVIFSSTGRLYEY-SS 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH:
                                                                                                                                                                                                                                                        QSMTRTLERYQKFSYGGPDTAIQNKENELVQSSRNEYLK-----LKARVENLQRTQR 112
                                                                                                                                                                                                                                                                                                                                              MGRGRVELKRIENKINRQVTFAKRRNGLLKKAYELSVLCDAEVALIIFSNRGKLYEFCSG 60
                                                                                 KL----EESNQLHGQVWEHGATLLGYERQSPHAVQQVPPHGGNGFFHSLEAAAEPT-LQI
                                                                                                                                                                                                                                                                                                                                                                                                                                    94;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    amino acid
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June 2, 1997
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37.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
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                                                                                                                                                                                                                                                      Sequence 4, Application US/08659188 Patent No. 6002069
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                                                                                                                                                                                                                                   GENERAL INFORMATION:
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LENGTH: 253 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
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COMPUTER READABLE FORM
                                                                                                                                 CORRESPONDENCE ADDRESS:
                                                                                                                                                     NUMBER OF SEQUENCES:
                                                                                                                                                                            TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                         181 AQQEQWDEQNH-----GHNMPPPPP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 SPKELQNLEQQLDTALKHIRSRKNQLMYDSINELQRKEKAIQEQNSMLSKQIKERENVLR 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          119 NVKELQSLENQLETSLRGVRAKKDHLLIDEIHDLNRKASLFHQENTDLYNKI----NLIR 174
                                                       CITY: San Diego
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-UD 1927
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CLASSIFICATION:
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                                                                                                STREET:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OPERATING SYSTEM: PC-DOS/MS-DOS
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                    ZIP:
                                                                                                                ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                QENDELHKKIYETEGPSGVNRESPTPFNFAVVETRDVPVQLELSTLPQQNNIE 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SCMEKILERYERYSYAERQLIAPESDSNTNWSMEYNRLKAKIELLERNQRHYLGEDLQAM 120
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                                                                                              4370 La Jolla Village Drive, Suite 700
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4370 La Jolla Village Drive, Suite 700
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                                                                                                                                                                                                               Yanofsky,
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                                                                                                                  Campbell and Flores
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                                                                                                                                                                            Reproductive Development and Methods of Making Same
                                                                                                                                                                                              Seed Plants Exhibiting Inducible Early
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                                                                                                                                                                                                                   Martin F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US/08/592,214A
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Best Local Similarity
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                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0.
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Yanofsky, Martin F.
TITLE OF INVENTION: Maize and Cauliflower APETALA1 Gene
TITLE OF INVENTION: Products and Nucleic Acid Molecules Encoding Same
               CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn
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                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         181 AQQEQWDEQNH-----GHNMPPPPP-----
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SOFTWARE: PatentIn Release #1.0, Version #1.25
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                                                                                                                                                                                                                                                                                      CITY: San Diego
STATE: California
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REGISTRATION NUMBER:
                                                                                FILING DATE:
                                                                                                 APPLICATION NUMBER:
                                                                                                                                                                                                                                                                   COUNTRY:
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                                                                                                                                          PatentIn Release #1.0, Version #1.25
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                                                                                05-JUN-1996
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Cathryn A.
BER: 31,815
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Pred. No. 1e-29;
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Best Local
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
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STREET: 40...
CITY: San Diego
CTATE: California
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APPLICANT: Weigel, Detlef
TITLE OF INVENTION: Seed
TITLE OF INVENTION: Devel
                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: Cambell, Cathryn A.
REGISTRATION NUMBER: 31.815
REFERENCE/DOCKET NUMBER: P-UD 1894
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
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MEDIUM TYPE: Floppy disk
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                                                                                                                                                        SEQUENCE CHARACTERISTICS:
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    MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: FILING DATE: 05-JUI CLASSIFICATION: CLASSI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE:
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                                         TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MGRGRVQLKRIENKINRQVTFSKRRAGLMKKAHEISVLCDAEVALVVFSHKGKLFEYSTD 60
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4370 La Jolla Village Drive, Suite 700
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              UMBER: US/08/655,241
05-JUN-1996
protein
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                                                                                                   US-09-149-976-4
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; Patent No. 6127123
Query Match
Best Local Similarity
Matches 83; Conserv
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                                                                                                                                                                     TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 253 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Yanofsky, Martin F.
TITLE OF INVENTION: Cauliflower Floral Meristem Identity
TITLE OF INVENTION: Genes and Methods of Using Campa
                                                                                                                    MOLECULE TYPE:
                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION: TELEPHONE: (619) 535-9001
                                                                                                                                                                                                                                                                                                                                      FILING DATE: 26-JAN-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/592,214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: FILING DATE: 09-SE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                      TOPOLOGY:
                                                                                                                                                       TYPE:
                                                                                                                                                                                                                                               TELEPHONE:
                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: P-UD 3291
                                                                                                                                                                                                                                                                                                       REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn Release #1.0, Version #1.25
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   32.3%; Score 393; DB 3
35.6%; Pred. No. 1e-29;
tive 56; Mismatches
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Pred. No. 1e-29;
                                          DB 3; Length 253;
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         62;
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                                                                                                                                                                                                                    Query Match 32.3%; Score 393; DB 4; Length 253; Best Local Similarity 35.6%; Pred. No. 1e-29; Matches 83; Conservative 56; Mismatches 62; Indels
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TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 05-JUN-1996
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn /
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
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APPLICATION NUMBER: US 08/659,188
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES:
                119 NVKELQSLENQLETSLRGVRAKKDHLLIDEIHDLNRKASLFHQENTDLYNKI----NLIR 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  181 AQQEQWDEQNH-----GHNMPPPPP-----
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                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 253 amino acids TYPE: amino acid TOPOLOGY: linear
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                                                               61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                               61 S-MKSVIDRYGK-AKEEQQVVANPNSELKFWQREAASLRQQLHNLQENYRQLTGDDLSGL 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REGISTRATION NUMBER: 31, REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: San Diego
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
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                                                                                                                                       1 MGRGRVQLKRIENKINRQVTFSKRRAGLMKKAHEISVLCDAEVALVVFSHKGKLFEYSTD 60
                                                                                                                                                          1 MGRGKIVIRRIDNSTSRQVTFSKRRNGIFKKAKELAILCDAEVGLVIFSSTGRLYEYSST 60
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                                                           SCMEKILERYERYSYAERQLIAPESDSNTNWSMEYNRLKAKIELLERNQRHYLGEDLQAM 120
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VENTION: Seed Plants Exhibiting Inducible Early
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BER: 31,815
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model
Run on:
Run on:
Run on:
Search time 43.45 Seconds
(without alignments)
530.758 Million cell updates/sec
Ritle:
Perfect score:
1216
Sequence:
1216
Sequence:
1216
Secoring table:
128138 seqs, 96089334 residues
Total number of hits satisfying chosen parameters:
283138
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR\_71:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

## SUMMARIES

29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10	9	8	7	6	5	4	ω	2	1	No.	Result	
401	401	402.5	402.5	402.5	403	405	405	408.5	409.5	414	416	417	417.5	418.5	419.5	420	425	426.5	426.5	428.5	435	589	605	636.5	638.5	643.5	666	729.5	Score		
ω.	ω ·	ω.	w	ω.	ω.	ω	·	·	ω ·						34.	34.	w	35.	35.	35.	35.	48.	49.	52.	52.	52.	54.8	0	Match	Query	æ
257	248	242	242	236	265	254	248	248	248	258	229	246	242	252	230	262	261	284	284	222	261	239	240	234	234	227	228	234	Length		
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S53306	T04170	T09571	T10486	S59480	T02261	T10185	A39534	T07185	T03592	G84858	T08040	E39534	JQ2212	A43484	T04000	T08039	T09603	A85214	T05033	S51934	S51935	T45801	T09700	A84515	T52100	H84614	T05621	T17029	ID		
MADS box protein M	MADS box protein -	MADS box protein M	MADS box protein -	MADS-box protein 3	MADS box protein -	MADS-box protein C	C	floral homeotic pr	floral homeotic pr	floral homeodomain	MADS-box protein -	floral homeotic pr	pr	probable transcrip	MADS-box protein A	MADS-box protein -	MADS-box protein 3	floral homeotic pr	floral homeotic pr	MADS-box protein d	probable MADS-box	MADS-box transcrip	MADS-box protein -	probable MADS-box	MADS-box transcrip	probable MADS-box	MADS-box protein A	MADS-box transcrip	Description		

MADS-box protein AGL17 homolog F20D10.60 - Arabidopsis thaliana C:Species: Arabidopsis thaliana (mouse-ear cress) C:Species: Arabidopsis thaliana (mouse-ear cress) C:Date: 23-Apr-1999 #sequence\_revision 23-Apr-1999 #text\_change 26-Aug-1999 C:Accession: T05C21 C:Accession: T05C21 R:Bevan, M.; Wedler, H.; Kutzner, M.; Wambutt, R.; Bancroft, I.; Mewes, H.W.; Mayer, submitted to the Protein Sequence Database, February 1999

A; Reference number: 215420 A; Accession: T05621 A; Molecule type: DNA A; Residues: 1-228 <BEV>

44	43	42	41	40	39	38	37	36	ω 5	34	ယ	32	31	30
383 381.5	383.5	384	385	385	385.5	386.5	390	390.5	391.5	392	393	394.5	399.5	401
31.5 31.4	31.5	31.6	31.7	31.7	31.7	31.8	32.1	32.1	32.2	32.2	32.3	32.4	32.9	33.0
256 219	225	250	273	253	254	227	247	242	239	286	246	250	248	259
22	2	N	N	2	2	N	N	Ν	N	N	Ν	2	2	8
\$27109 \$46526	T04168	T07100	T03410	S57586	S52236	S23730	S60307	S71208	A44343	JQ2289	T17023	T04167	S20886	T01700
MADS box protein A MADS box protein m	xod	xod	MADS box protein -	-pos	xod	bos	pro	xod	promotes sex organ	al h	MADS box protein 1	xod	MADS box protein s	hypothetical prote

## ALIGNMENTS

T17029 T17029 T17029 T17029 C;Bate: Internation factor DEFH125 - garden snapdragon C;Species, Antirrhinum majus (garden snapdragon) C;Accession: T17029 C;Accession: T17029 C;Accession: T17029 T17029 T17020 C;Accession: T17029 T17020
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A;Cross-references: I
A;Experimental source
C;Genetics:
A;Map position: 4
A;Introns: 61/2; 87/:
A;Note: F20D10.60
C;Superfamily: trans(F;2-57/Domain: serum
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C;Superfamily: transcription factor squa;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    probable MADS-box protein AGL17 [imported] - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 002-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 1:C;Accession: H84614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Reference number: A84420; A; Accession: H84614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Qy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Residues: 1-227 <STO>
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   181 YKKAYGTSNTNGLGHHELVD--
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                                 HKKIYETEGPSGVNRESPTPFNFAVVETRDVPVQLELSTLPQQNNIEPST
                                                                     KELQNIESQLEMSLRGIRMKREQILTNEIKELTRKRNLVHHENLELSRKVQRIHQENVEL
                                                                                                        KELQSLENQLETSLRGVRAKKDHLLIDEIHDLNRKASLFHQENTDLYNKINLIRQENDEL 180
                                                                                                                                           SVKSTIERFNTAKMEEQELMNPASEVKFWQREAETLRQELHSLQENYRQLTGVELNGLSV
                                                                                                                                                                           SMKSVIDRYGKAKEEQQVVANPNSELKFWQREAASLRQQLHNLQENYRQLTGDDLSGLNV 120
                                                                                                                                                                                                                MGRGKIVIQKIDDSTSRQVTFSKRRKGLIKKAKELAILCDAEVCLIIFSNTDKLYDFASS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MGRGKIVIRRIDNSTSRQVTFSKRRNGIFKKAKELAILCDAEVGLVIFSSTGRLYEYSST 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YKKAYMANTNGFTHRE-----VAVADDESHTQIRLQLS---QPEHSDYDTPPR 225
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KELQSLENQLETSLRGVRAKKDHLLIDEIHDLNRKASLFHQENTDLYNKINLIRQENDEL 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SMKSVIDRYGKAKEEQOVVANPNSELKFWQREAASLRQQLHNLQENYRQLTGDDLSGLNV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NELNSLENQIEISLRGIRMRKEQLLTQEIQELSQKRNLIHQENLDLSRKVQRIHQENVEL 180
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                                                                                                                                                                                                                                                                                         Conservative
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-AVYESH-AQVRLQLSQ-PEQSHYKTSS
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                                                                                                                                                                                                                                                                                                          Score 643.5; DB 2
Pred. No. 9.9e-37;
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Pred. No. 3e-38;
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A; Gene: At2g14210
A; Map position: 2
C; Superfamily: transcription
                                                                                                                                                                                                                                                                       R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fuji M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Teuss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Nature 402, 761-768, 1999
                                                                       C; Genetics:
                                                                                                   A; Cross - references:
                                                                                                                        A; Molecule type: DNA
A; Residues: 1-234 <STO>
                                                                                                                                                                                                  A; Reference number: A84420; A; Accession: A84515
                                                                                                                                                                                                                         A; Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana A; Reference number: A84420; MUID:20083487
                                                                                                                                                                                                                                                                                                                                                                      probable MADS-box protein ANR1 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 16-Feb-2001
C;Accession: A84515
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Note: nitrit inducible C; Superfamily: transcription factor squa; C; Keywords: transcription factor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C; Genetics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R; Zhang, H.;
Science 279,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Description:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C; Function:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Gene: ANR1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Cross-references:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: mRNA
A; Residues: 1-234 < 2H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Status: preliminary; translated
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                                                                                                                                                                        Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    60 TSMKSVIDRYGKAKEEQQVVANPNSELKFWQREAASLRQQLHNLQENYRQLTGDDLSGLN 119
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279, 407-409, 1998
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                                                                                                 GB:AE002093;
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                                                                                                 NID: g4586018;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 638.5; DB 2
Pred. No. 2.3e-36;
7; Mismatches 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            from
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                                                                                                                                                                                                                                                                                                                  T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y hen, M.; VanAken, S.E.; Umayam, L.; Tallon,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PPQLQLIQLQPAPREKSI - -
                                                                                                 PIDN: AAD25638.1;
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                                                                                                 GSPDB:GN00139
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    submitted to the EMBL Data Library, March 1997
A;Reference number: 216825
A;Accession: T09700
A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MADS-box protein - alfalfa (fragment)
C;Species: Medicago sativa (alfalfa)
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 11-Jan-2000
C;Accession: T09700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Qy
C; Accession: T45801
R; Benes, V.; Rechman
submitted to the Pro
                                                              MADS-box transcription factor-like protein - Arabidopsis thaliana N;Alternate names: protein F2809,80 C;Species: Arabidopsis thaliana (mouse-ear cress) C;Species: Arabidopsis thaliana (mouse-ear cress)
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C;Superfamily: transcription factor squa; serum response factor DNA-binding domain homo.
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A; Residues: 1-240 < DUN>
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                                                                                                                                                                                                                                     167 KVYGTKDKNGTNRVLSLTNGVGIGDDSNRTCESPAQ---PATETRTTTALMHSLEISVL 222
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MGRGKIVIRRIDNSTSRQVTFSKRRSGLLKKAKELSILCDAEVGVIIFSSTGKLYDVASN 60
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                                                                                                                                                                                                                                                                                                                                                LQSLENQLETSLRGVRAKKDHLLIDEIHDLNRKASLFHQENTDLYNKINLIRQENDELHK 182
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135; Conserv
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                      Rechmann, S.;
  the Protein Sequence
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54.9%;
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                      Borkova,
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Pred. No. 3.1e-36;
    Database,
                        D.;
                      Ansorge, W.;
                                                                                                                                                                                                                                                                              -ESPTPFNFAVVETRDVPV---QLELSTL 220
    January
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                      Mewes, H.W.; Lemcke,
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                        Mayer, K.
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A; Molecule type: DNA
A; Residues: 1-239 <BEN>
A; Cross-references: EMBL: AL137080
                                                                                                                                                             C;Superfamily: transcription factor squa; serum response factor DNA-binding C;Keywords: DNA binding; transcription regulation F;2-57/Domain: serum response factor DNA-binding domain homology <SRF>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Title: Conifer homologues to genes that control floral development A;Reference number: S51934; MUID:95170009
A;Accession: T14846
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     probable MADS-box protein dall - Norway spruce
C;Species: Picea abies (Norway spruce)
C;Date: 14-Jul-1995 #sequence_revision 01-Dec-2000 #text_change 01-Dec-2000
C;Accession: T14846; S51935
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S51935
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C; Superfamily: transcription factor squa; serum response factor DNA-binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Map position: 3
A; Introns: 61/2;
A; Note: F2809.80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Experimental source: cultivar Columbia; BAC clone F2809
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Accession: T45801
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Reference number: 223014
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R;Tandre, K.; Albert, V.A.; Sundas, A.; Engstroem, P. plant Mol. Biol. 27, 69-78, 1995
γ
                                                                                                                                                                                                                                                                                    A; Molecule type: DNA
A; Residues: 92-156 <TA2>
                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: mRNA
A; Residues: 1-261 <TAN>
                                                                                                                                                                                                                                       A;Gene: dall
                                                                                                                                                                                                                                                              C; Genetics:
                                                                                                                                                                                                                                                                                                                                                    A; Accession: S51935
                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: EMBL:X80902; NID:g695685; PIDN:CAA56864.1; PID:g695686
                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             171 NLIRQENDELHKKIYETEGPSGVNRESPTPFNFAVVETRDVPVQLELSTLPQQNNIEPST 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      111 TGDDLSGLNVKELQSLENQLETSLRGVRAKKDHLLIDEIHDLNRKASLFHQENTDLYNKI 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61
                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MGRGKIAIKRINNSTSRQVTFSKRRNGLLKKAKELAILCDAEVGVIIFSSTGRLYDFSSS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MGRGKIVIRRIDNSTSRQVTFSKRRNGIFKKAKELAILCDAEVGLVIFSSTGRLYEYSST 60
  1 MGRGKIVIRRIDNSTSRQVTFSKRRNGIFKKAKELAILCDAEVGLVIFSSTGRLYEYSST 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AIQL 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APKL 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NLMHQQNMELHEKVSEVEGVKIANKNSLLTNGLDMRDTSNEHVHLQLSQ-PQHDHETHSK 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MGEELSGLSVEALQNLENQLELSLRGVRMKKDQMLIEEIQVLNREGNLVHQENLDLHKKV 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SMKSVIERYSDAKGETSSENDPASEI------QEMYIVTLEKYAYSEELVLDRQM 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SMKSVIDRYGKAKEEQQVVANPNSELKFWQREAASLRQQLHNLQ-ENY------RQL 110
                                                                                                                                                                                                                                                                                                                                preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             130;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    w
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           87/3; 140/3; 154/3; 182/3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    48.4%;
                                                                       35.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             39;
                                                                       Score 435; DB 2;
Pred. No. 1.6e-22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 589; DB 2;
Pred. No. 5.2e-33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                      Mismatches
                                                      69;
                                                      Indels
                                                      40;
                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            in anglosperms
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      domain
                                                                                                                                                                                                                      domain
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RESULT 10
T0503T
T0503T
Horal homeotic protein agamous - Arabidopsis thaliana (fragment)
H.Alternate names: probable transcription factor agamous; protein F13C5.130
C.Specles: Arabidopsis thaliana (mouse-ear cress)
C.Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 20-Jun-2000
C.Accession: T05033; S10933
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Gene: dal2
C;Superfamily: transcription factor squa; serum response factor DNA-biC;Keywords: DNA binding; transcription regulation
E;2-57/Domain: serum response factor DNA-binding domain homology <SRF>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R;Tandre, K.; Albert, V.A.; Sundas, A.; Engstroem, P.
Plant Mol. Biol. 27, 69-78, 1995
A;Title: Conifer homologues to genes that control floral development in angiosperms.
A;Reference number: S51934; MUID:95170009
A;Accession: T14847
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Species: Picea abies (Norway spruce)
C;Date: 14-Jul-1995 #sequence_revision 01-Dec-2000 #text_change 01-Dec-2000
C;Accession: T14847; S51934
A; Reference number: Z15395
A; Accession: T05033
A; Molecule type: DNA
                                                                                       R; Bevan, M.; Pohl, T.; We submitted to the Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DЬ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 9
S51934
MADS-box protein dal2 - Norway spruce
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: DNA
A; Residues: 92-156 <TA2>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Accession:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Experimental source: female cone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: EMBL:X79280; NID:g695687; PIDN:CAA55867.1; PID:g695688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Status: preliminary; translated from GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Residues:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Superfamily: transcription factor squa; serum response factor DNA-binding; keywords: DNA binding; transcription regulation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 118 LNVKELQSLENQLETSLRGVRAKKDHLLIDEIHDLNRKASLFHQENTDLYNKI 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 SVKRTIERYKKTCVDNNHGGVISESNSQ--YWQQEAGKLRQQIEILQNANRHLMGDGLTA 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MGRGKIEIKRIENTTNRQVTFCKRRNGLLKKAYELSVLCDAEVALIVFSSRGRLYEFANH 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MGRGKIVIRRIDNSTSRQVTFSKRRNGIFKKAKELAILCDAEVGLVIFSSTGRLYEYSST 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            --NIEPSTAPKLGLQLIP 240
                                                                                                                                                                                                                                                                                                                                                                                                          LNIKELKQLEVRLEKGIGRVRSKKNEMLLEEIDIMQRREHILIQENEILRSKI 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SMKSVIDRYGKAKEEQQ----VVANPNSELKFWQREAASLRQQLHNLQENYRQLTGDDLSG 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HVDCEPTL--QIGYQPVP 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VKELQQLERQLEVALAHLRSRKTQVMLDQIEELRQRERLLH--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LQKKLSETEGRDVITGIEQTSNTNTGTNGPWDSSITNT-----AYALSH-PQQNSNASLH 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LHKKIYETEGP---SGVNRESPT-----PFNFAVVETRDVPVQLELSTLPQQN-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VKELQSLENQLETSLRGVRAKKDHLLIDETHDLNRKASLFHQENTDLYNKINLIRQENDE 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SMNKTLERYEKCSYAMQDTTGVSDREAQNWHQEVTKLKGKVELLQRSQRHLLGEDLGPLN 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SMKSVIDRYGKAK-EEQQVVANPNSELKFWQREAASLRQQLHNLQENYRQLTGDDLSGLN 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1-222 <TAN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              h 35.2%; score 428.5; DB 2; similarity 50.9%; Pred. No. 3.6e-22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      S51934
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                            T.; Weizenegger,
                                                                                       Sequence Database,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         35;
                                                                                                               T.; Bancroft, I.; Mewes, H.W.; Mayer, K.F.X.; Schue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                       February 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         45;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 222;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5,
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Matches Query Match

102;

Conservative

Local Similarity

35.1%; Score 426.5; DB 2; 41.1%; Pred. No. 6.8e-22; ... wismatches 74;

Length 284;

Indels

23;

Gaps

7;

```
floral homeotic protein agamous [imported] - Arabidopsis thaliana C:Species: Arabidopsis thaliana (mouse-ear cress) C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 02-Mar-2001 C:Accession: A85214 R;anonymous, The European Union Arabidopsis Genome Sequencing Consortium, T Nature 402, 769-777, 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Description: probably involved in regulating genes that determine stamen and carpel c;Superfamily: transcription factor squa; serum response factor DNA-binding domain ho C;Keywords: DNA binding; nucleus; transcription factor; transcription regulation E;50-105/Domain: serum response factor DNA-binding domain homology <SRF>
C; Superfamily: transcription factor squa; serum response
                                                                                                                 A;Residues: 1-284 <STO>
A;Cross-references: GB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Note: intron positions not resolved A; Note: F13C5.130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: mRNA
A; Residues: 'H', 1-284 < YAN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Reference number: S10933; A; Accession: S10933
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Title: The protein encoded by the Arabidopsis homeotic gene agamous resembles trans A;Reference number: S10933; MUID:90309968
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Experimental source: cultivar Columbia; BAC clone F13C5 R; Yanofsky, M.F.; Ma, H.; Bowman, J.L.; Drews, G.N.; Feld Nature 346, 35-39, 1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Residues: 1-284 <BEV>
A;Cross-references: EMBL:AL021711
                            A; Map position:
                                                  A; Gene: AT4g18960
                                                                                        C; Genetics:
                                                                                                                                                                          A; Molecule type: DNA
                                                                                                                                                                                                          A; Status: preliminary
                                                                                                                                                                                                                                      A; Accession: A85214
                                                                                                                                                                                                                                                                A; Reference number: A85001; MUID: 20083488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A85214
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                                                                                                                                                                                                                                                                                                  A; Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              110 VKGTIERYKKAISDNSNTGSVAEINAQ--YYQQESAKLRQQIISIQNSNRQLMGETIGSM 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     277 DQTALQLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             224 RNNPSISLMPGGSNYEQLMPPP---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               168 SPKELRNLEGRLERSITRIRSKKNELLFSEIDYMQKREVDLHNDNQILRAKI----AENE 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      62 MKSVIDRYGKAKEEQQ----VVANPNSELKFWQREAASLRQQLHNLQENYRQLTGDDLSGL 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      50 GRGKIEIKRIENTTNRQVTFCKRRNGLLKKAYELSVLCDAEVALIVFSSRGRLYEYSNNS 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ELHKKIYETEGPSGVNRESPTPFNFAVVETRDVPVQ----LELSTLPQQNNIEPSTA---
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                                                                                                                    GB:NC_001268; NID:g7268690; PIDN:CAB78898.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       35.18;
41.18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 426.5; DB z;
Pred. No. 6.8e-22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QTQSQPFDSRNYFQVAAL-QPNNHHYSSAGRQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length
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factor DNA-binding
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C:Species: Cucumis sativus (cucumber)
C:Date: 21-May-1999 #sequence_revision 21-May-1999 #text_change 08-Oct-1999
C:Accession: T08039
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MADS-box protein 3 - Monterey pine
C:Species: Pinus radiata (Monterey pine)
C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jan-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C; Accession: TO
R; Mouradov, A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Qγ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Cross-references: EMBL: U76726; NID: g2160700; PID: g2160701
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A; Accession: T09603
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                          R;Kater,
                                                                                                     MADS-box protein - cucumber
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Best Local S
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  M.M.; Colombo,
11 10, 171-182,
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                                                                                                                                                                                                                                                                                                                                     VKELQSLENQLETSLRGVRAKKDHLLIDEIHDLNRKASLFHQENTDLYNKINLIRQENDE 179
                                                                                                                                                                                                                                                                                                                                                                            SMNKTLERYEKCSYAMODTTGVSDREAQNWHQEVTKLKGKVELLQRSQRHLLGEDLGPLN 120
                                                                                                                                                                                                                                                                                                                                                                                                                 SMKSVIDRYGKAK-EEQQVVANPNSELKFWQREAASLRQQLHNLQENYRQLTGDDLSGLN 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                          MGRGRVQLRRIENKINRQVTFSKRRNGLLKKAYELSVLCDAEVALIIFSTRGKLYEFASS 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ELHKKIYETEGPSGVNRESPTPFNFAVVETRDVPVQ----LELSTLPQQNNIEPSTA---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GRGKIEIKRIENTTNRQVTFCKRRNGLLKKAYELSVLCDAEVALIVFSSRGRLYEYSNNS 109
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                                                                                                                                                                                                              LQKKLSETEGRDVITGIEQTSNTNTGTNGPWDSSITNT
                                                                                                                                                                                                                                                                                            VKELQQLERQLEVALTHLRSRKTQVMLDQIEELRQRERLLH:
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                       Franken, J.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 425; DB 2; Pred. No. 7.7e-22;
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                     Busscher, M.; Masiero,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 261;
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                   S.; van Lookeren Campagn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24;
                                                                                                                                                                                                                                                                                            EVNKS 166
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C;Accession: T04000
R;Bevan, M.; Murphy, G.; Ridley, P.; Hudson, submitted to the Profesin Sequence Database, J
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                                                                                                                                                C; Superfamily: transcription factor squa; serum response factor DNA-binding C; Keywords: DNA binding F; 2-57/Domain: serum response factor DNA-binding domain homology <SRF>
                                                                                                                                                                                                                 A; Introns: 61/2;
A; Note: T5L19.90
                                                                                                                                                                                                                                                                                                    C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: DNA
A; Residues: 1-230 <BEV>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N;Alternate names: protein T5L19.90
C;Species: Arabidopsis thaliana (mouse-ear cress)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Дβ
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A; Residues: 1-262 <KAT>
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                                                                                                                                                                                                                                                       A; Map position: 4
                                                                                                                                                                                                                                                                                A; Gene: AGL11
                                                                                                                                                                                                                                                                                                                          A; Experimental source: cultivar Columbia; BAC
                                                                                                                                                                                                                                                                                                                                            A; Cross-references: EMBL: AL049481
                                                                                                                                                                                                                                                                                                                                                                                                             A; Accession: T04000
                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Reference number: Z15184
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1 MGRGKIVIRRIDNSTSRQVTFSKRRNGIFKKAKELAILCDAEVGLVIFSSTGRLYEYSST 60
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                                                                Similarity
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                                              Conservative
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                                                                34.5%; Score 419.5; DB 2
45.0%; Pred. No. 1.5e-21;
                                            42; Mismatches
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61 SMKSVIDRYGKAKEEQ---QVVANPNSELKFWQREAASLRQQLHNLQENYRQLTGDDLSG 117

MGRGKIEIKRIENSTNRQVTFCKRRNGLLKKAYELSVLCDAEVALIVFSTRGRLYEYANN

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probable transcription factor BAG1 - rape
C;Species: Brassica napus (rape)
C;Date: 10-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 24-Sep-1999
C;Accession: A43484
R;Mandel, M.A.; Bowman, J.L.; Kempin, S.A.; Ma, H.; Meyerowitz, E.M.; Yanofsky, M.F.
Cell 171, 133-143, 1992
A;Fitle: Manipulation of flower structure in transgenic tobacco.
A;Reference number: A43484
A;Reference number: A43484, MUID:93008236
A;Accession: A43484
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: nucleic acid
A;Residues: 1-252 <ANAN-
A;Cross-references: GB:M99415; NID:9167125; PIDN:AAA32985.1; PID:9167126
A;Note: sequence extracted from NCBI backbone (NCBIP:115468)
C;Superfamily: transcription factor squa; serum response factor DNA-binding domain homol
C;Keywords: DNA binding; nucleus; transcription regulation
F;18-73/Domain: serum response factor DNA-binding domain homol
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Best Local Similarity
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                                                                                                                                                      223 QNNIEPSTA---PKLGLQLI 239
                                                                                                                                                                                                                                                                                                                            119 NVKELQSLENQLETSLRGVRAKKDHLLIDEIHDLNRKASLFHQENTDLYNKINLIRQEND 178
                                                                                                                                                                                                                                                                                                                                                                   61 NIRSTIERYKKACSDSTNTSTVQEINA--AYYQQESAKLRQQIQTIQNSNRNLMGDSLSS 118
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                                                                                                           PNNHHYSSAGREDQTALQLV 252
                                                                                                                                                                                                 LLRAKIAENERNNPSMSLMPGGSNYEQIMPPPQTQPQPF
                                                                                                                                                                                                                                        ELHKKIYETEG-----PSGVNRE-----SPTPFNFAVVETRDVPVQLELSTLPQ 222
                                                                                                                                                                                                                                                                                   SPKELRNLEGRLDRSVNRIRSKKNELLFAEIDYMQKR-----EVDLHN-----DNQ 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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      Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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E Agamous-like MADS box protein At493740.  8 Arabidopsis thaliana (Mouse-ear cress).  6 Eukaryota: Viridiplantae; Streptophyta: Embryophyta: Tracheophyta: Celkaryota: Viridiplantae; Streptophyta: Embryophyta: Core eudicots: Rosidae centrosids II. Brassicales: Streptophyta: Mapholopsis.  8 MABL_TRAIN=3702:  9 ESDUENCE FROM N.A.  10 ESTAIN=CV. COLUMBIA:  11 Expansional Columbia: Stiekema W., Entian KD., Terryn N., And Harris B., Ansorge W., Brandt P., Grivell L.A., Rieger M., Mayer K.F.X., Schueller C., Wambutt R., Murphy G., Volckmert G., And Harris B., Ansorge W., Brandt P., Grivell L.A., Rieger M., Mayer K.F.X., Schueller C., Wambutt R., Murphy G., Volckmert G., And Harris B., Ansorge W., Brandt P., Grivell L.A., Rieger M., Mache R., Muchlar N., Delseny M., Pulgdomenech P., Watson M., Schmidtheini T., And Kreis M., Delseny M., Pulgdomenech P., Watson M., Schmidtheini T., And Kreis M., Delseny M., Pulgdomenech P., Watson M., Schmidtheini T., And Kreis M., Delseny M., Pulgdomenech P., Watson M., Schmidtheini T., And Weitheelgartner M., McDullagh B., Bliham L., Robben J., Vandenbussche F., Andersonger T., Bothe G., Ramsperger U., Hilbert H., Ridley P., And Menter B., Porteet B., Porteet M., Bastiaens I., Aert R., Defoor E., Watson M., Weller T., Bothe G., Ramsperger U., Hilbert H., Braun M., Meller R., Peters S., Van Staveren M., Dirkse W., Molzer E., Brandt A., Peters S., Van Staveren M., Dirkse W., Molzer E., Brandt A., Peters S., Van Staveren M., Dirkse W., Molzer S., Brandt A., Peters S., Van Staveren M., Dirkse W., Molzer S., Brandt A., Peters S., Van Staveren M., Dirkse W., Molzer S., Brandt A., Peters S., Van Staveren M., Dirkse W., Molzer S., Brandt M., McLay K., Mayes R., Mayes	228 AA. update) update)	WT'S
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Agamous-like MADS box protein AGL17.
AGL17 OR AT2G22630 OR T9122.7.
Arabidopsis thaliana (Mouse-ear cress).
Bukaryota; Viridiplantae, Streptophyta;
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"Diverse roles for MADS box genes in Arabidopsis development.";
Plant Cell 7:1259-1269(1995).
-i- FUNCTION: PROBABLE TRANSCRIPTION FACTOR.
-i- SUBCELLULAR LOCATION: Nuclear (By similarity).
-i- TISSUE SPECIFICITY: PREFRENTIALLY EXPRESSED IN ROOTS.
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PROSITE; PS50066; MADS_BOX_2; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mendel; 6456; Arath; MADS; 6456.
Mendel; 39770; Arath; MADS; 39770.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; U20186;
HSSP; P11746;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.";
121 KELQSLENQLETSLRGVRAKKDHLLIDEIHDLNRKASLFHQENTDLYNKINLIRQENDEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR002487; K-box.
InterPro; IPR002100; MADS-box
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TRANSFAC; T03020;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=96004530; PubMed=7549482;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 8-227 FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nature 402:761-768(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Venter J.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      eurosids II; Brassicales; Brassicaceae; Arabidopsis NCBI_TaxID=3702;
                                                                   61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIMILARITY: BELONGS TO THE MADS DOMAIN FAMILY
                                                                                                                                                                             MGRGKIVIQKIDDSTSRQVTFSKRRKGLIKKAKELAILCDAEVCLIIFSNTDKLYDFASS
                                                                                                                                                                                                                                    MGRGKIVIRRIDNSTSROVTFSKRRNGIFKKAKELAILCDAEVGLVIFSSTGRLYEYSST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FACTORS
                                                                                           SMKSVIDRYGKAKEEQQVVANPNSELKFWQREAASLRQQLHNLQENYRQLTGDDLSGLNV 12C
                                                         SVKSTIERFNTAKMEEQELMNPASEVKFWQREAETLRQELHSLQENYRQLTGVELNGLSV 120
                                                                                                                                                                                                                                                                                                 131;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AC006340; AAD15571.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                              227 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LANDSBERG ERECTA; TISSUE=Root;
                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 regulation; DNA-binding; Nuclear protein.
3 57 MADS.
95 167 K-BOX.
11 227 AVYESHAOVRLOLSOPEOSHVKTSCN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1MNM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAC49084.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                              26314 MW;
                                                                                                                                                                                                                                                                                                                       52.9%; Score 643.5; DB 1
57.0%; Pred. No. 6.5e-36;
                                                                                                                                                                                                                                                                                                 46; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CS (IN REF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AVYESHAQVRLQLSQPEQSHYKTSSNS
                                                                                                                                                                                                                                                                                                                                                                                                                                              2C02283974D76594 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          There are no restrictions ng as its content is in
                                                                                                                                                                                                                                                                                                                                                        DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Usage by
                                                                                                                                                                                                                                                                                                 48;
                                                                                                                                                                                                                                                                                                                                                     Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OF
                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TRANSCRIPTION
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                                                                                                                                                                                                                                                                                           Gaps
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RESULT
AG_ARATH
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Best Local Sin Matches 102;
                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ALADIGOPSIS thaliana (Mouse-ear cress).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosia; eurosids II; Brassicales: Rrassicano
                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                    "The protein encoded by the Arabidopsis resembles transcription factors."; Nature 346:35-39(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=CV. LANDSBI
MEDLINE=90309968;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15-DEC-1998 (Rel.
16-OCT-2001 (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AG_ARATH
                                                                                                                                                                                                                                               entities requires a license agreement (Some or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AGAMOUS
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                                                                                                                                                                                                                                                                      modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                     DOMAIN
                                                                                              Transcription
                                                                                                        PROSITE; PS00350; MADS_BOX_1; 1.
PROSITE; PS50066; MADS_BOX_2; 1.
                                                                                                                                         PRINTS;
                                                                                                                                                  Pfam; PF01486; K-box; 1. Pfam; PF00319; SRF-TF; 1.
                                                                                                                                                                     InterPro; IPR002487; K-box.
InterPro; IPR002100; MADS-box.
                                                                                                                                                                                            TRANSFAC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Meyerowitz E.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Yanofsky M.F., Ma H., Bowman J.L., Drews G.,
                                                                           DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               181 YKKAYGTSNTNGLGHHELVD---AVYESH-AQVRLQLSQ-PEQSHYKTSS 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 KELQNIESQLEMSLRGIRMKREQILTNEIKELTRKRNLVHHENLELSRKVQRIHQENVEL 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   181 HKKIYETEGPSGVNRESPTPFNFAVVETRDVPVQLELSTLPQQNNIEPST 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ω
                                                                                                                                                                                                                                                                                                                                               SIMILARITY: CONTAINS A PROBABLE DIMERIZATION DOMAIN FOUND IN
                                                                                                                                                                                                                                                                                                                                                                                     SUBCELLULAR LOCATION: Nuclear.
MISCELLANEOUS: MUTATIONS IN THE AG GENE RESULT IN THE REPLACEMENT
OF THE SIX STAMENS BY SIX PETALS AND OF THE CARPELS BY A NEW
                                                                                                                                                                                                                                                                                                                                                                    SIMILARITY: BELONGS
                                                                                                                                                                                                                                                                                                                                                                                                                                  FUNCTION: PROBABLE TRANSCRIPTION GENES THAT DETERMINES STAMEN AND
                                                                                                                                                                                                                                                                                                                                    SRF-TYPE TRANSCRIPTION FACTORS (K-BOX).
                                                                                                                                                                                                                 ; x53579; CAA376
S10933; S10933.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P11746; 1MNM.
                                                                                                                             ; PR00404; MADSDOMAIN.
SM00432; MADS; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     protein.
           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LANDSBERG
                                                      252 AA;
 Conservative
                                                                                             regulation; DNA-binding; Activator; Nuclear protein.
                                                                                                                                                                                                                           CAA37642.1; ALT_INIT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ERG ERECTA;
PubMed=1973265;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                37, Last sequence update)
40, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15, Created)
                                                                         184
                                                      28723
          35.1%;
41.1%;
                                                                                                                                                                                                                                                                                                                                                                    TO
                                                      MW.
49;
                                                                                                                                                                                                                                                                                                                                                                    THE MADS
                                                               × ->
                                                                        K-BOX.
          Score 426.5;
Pred. No. 1.4
                                                                                    MADS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                    -> T (IN REF. 1).
4E7591AD85654C1C
 Mismatches
           No. 1.4e-21
                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                  FACTOR INVOLVED IN CARPEL DEVELOPMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               update)
                                                                                                                                                                                                                                                           (See http://www.isb-sib.ch/announce,
                                                                                                                                                                                                                                                                              There are no restrictions in as its content is in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           homeotic gene agamous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A
                    DB 1;
                                                                                                                                                                                                                                                                                                                                                                    FAMILY
                                                                                                                                                                                                                                                                      Usage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Feldmann K.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           core eudicots; Rosidae;
                                                    CRC64;
                                                                                                                                                                                                                                                                                                                                                                    OF.
                   Length
                                                                                                                                                                                                                                                                      by and
                                                                                                                                                                                                                                                                                                                                                                                                                                  REGULATING
IN WILD-TYPE
                     252;
23;
                                                                                                                                                                                                                                                                       tor
Gaps
                                                                                                                                                                                                                                                                       commercial
7;
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RESULT 4
AG11_ARATH
RA Langham S.-A., McCullagh B., Bilham L., Robben J.,
RA Langham S.-A., McCullagh B., Bilham L., Robben J.,
RA Wan der Schueren J., Grymonprez B., Chuang Y.-J., Vandenbussche F.,
RA Wan der Schueren J., Grymonprez B., Chuang Y.-J., Vandenbussche F.,
RA Hraeken M., Weltjens I., Voet M., Bastiaens I., Aert R., Defoor E.,
RA Weitzenegger T., Bothe G., Ramsperger U., Hilbert H., Braun M.,
RA Holzer E., Brandt A., Peters S., van Staveren M., Dirkse W.,
RA Mooijman P., Klein Lankhorst R., Rose M., Hauf J., Koetter P.,
RA Mooijman P., Klein Lankhorst R., Rose M., Hauf J., Koetter P.,
RA Mooijman P., Klein Lankhorst R., Rose M., Hauf J., Koetter P.,
RA Mooijman P., Klein Lankhorst R., Rose M., Hauf J., Koetter P.,
RA Berneiser S., Hempel S., Feldpausch M., Lamberth S., Van den Daele H.,
RA Berneiser S., Huge M., Grein A., Quail M., Bray-Allen S.,
RA Van Montagu M., Rogers J., Cronin A., Quail M., Bray-Allen S.,
RA Clark L., Doggett J., Hall S., Kay M., Lennard N., McLay K., Mayes R.,
RA Clark L., Doggett J., Hall S., Kay M., Lennard N., McLay K., Mayes R.,
RA Borkova D., Bloecker H., Scharfe M., Benes V., Rechmann S.,
RA Borkova D., Bloecker H., Scharfe M., Grimm M., Loehnert T.-H.,
RA Borkova D., Bloecker H., Scharfe M., Grimm M., Loehner D.,
RA Neumann S., Argiriou A., Vitale D., Liguori R., Piravandi E.,
RA Neumann S., Argiriou A., Vitale D., Liguori R., Piravandi E.,
RA Massenet O., Quigley F., Clabauld G., Muendlein A., Felber R.,
RA Chefdor F., Cooke R., Berger C., Monfort A., Casacuberta E.,
RA Gibbons T., Weber N., Vandenbol M., Bargues M., Terol J., Torres A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AG11_ARATH
Q38836;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Arabidopsis thaliana (Mouse-ear cress).
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosid
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kreis M., Del
Reichert B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mayer K.F.X., Schueller C., Wambutt R., Murphy G., Volckaert G., Pohl T., Duesterhoeft A., Stiekema W., Entian K.-D., Terryn N., Harris B., Ansorge W., Brandt P., Grivell L.A., Rieger M., Weichselgartner M., de Simone V., Obermaier B., Mache R., Mueller M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AGL11 OR AT4G09960
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Agamous-like MADS box
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Plant
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=96004530; PubMed=7549482;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=3702;
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16-OCT-2001 (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=20083488; PubMed=10617198;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        179
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2
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B., Portetelle D., Perez-Alonso M., Boutry M., Bancroft I.,
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PROSITE; PS50066; MADS_BOX_2; 1.
PROSITE; PS50066; MADS_BOX_2; 1.
Transcription regulation; DNA-binding; Nuclear protein.
DOMAIN 3 57 MADS.
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Pfam; PF00319; SRF-TF; 1.
PRINTS; PR00404; MADSDOMAIN.
SMART; SM00432; MADS; 1.
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-!- FUNCTION: PROBABLE TRANSCRIPTION FACTOR.
-!- SUBCELLULAR LOCATION: Nuclear (By similarity)
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179 QHHHQMVSGSE 189
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                                                                                                                                                                                                                           LNVKELQSLENQLETSLRGVRAKKDHLLIDEIHDLNRKASLFHQENTDLYNKINLIRQEN 177
                                                                                                                                                                                                                                                                                                         NIRSTIERYKKACSDSTNTSTVQEINA--AYYQQESAKLRQQIQTIQNSNRNLMGDSLSS
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Bielke C.,
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PROSITE; PS50066; MADS_BOX_2; 1.
Transcription regulation; DNA-binding; Activator; Nuclear protein.
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Brassica napus (Rape).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosid

eurosids II; Brassicales; Brassicaceae; Brassica.
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MEDLINE=93008236; PubMed=1356631;
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InterPro; IPR002100; MADS-box.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Manipulation of flower structure in transgenic tobacco.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Yanofsky M.F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mandel M.A., Bowman J.L., Kempin S.A., Ma H., Meyerowitz E.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                119 NYKELQSLENQLETSLRGYRAKKDHLLIDEIHDLNRKASLFHQENTDLYNKINLIRQEND 178
                                                                                                                                                                        62
                                                                                                               78
                                                                                                                                                                                                                              18
                                                                                                                                                                                                                                                                                 2 GRGKIVIRRIDNSTSRQVTFSKRRNGIFKKAKELAILCDAEVGLVIFSSTGRLYEYSSTS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIMILARITY: BELONGS TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SRF-TYPE TRANSCRIPTION FACTORS (K-BOX).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUBCELLULAR LOCATION: Nuclear
SPKELRNLEGRLDRSVNRIRSKKNELLFAEIDYMQKR
                                                                                                                                                                                                                              GRGKIEIKRIENTTNRQVTFCKRRNGLLKKAYELSVLCDAEVALIVFSSRGRLYEYSNNS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FLOWERS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENES THAT DETERMINES
                                                                                                                                                                  MKSVIDRYGKAKEEQQ----VVANPNSELKFWQREAASLRQQLHNLQENYRQLTGDDLSGL 118
                                                                                                         VKGTIERYKKAISDNSNTGSVAEINAQ--YYQQESAKLRQQIISIQNSNRQLMGETIGSM 135
                                                                                                                                                                                                                                                                                                                                                104;
                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       112
252 AA;
                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1MNM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26, Created)
26, Last sequence up
40, Last annotation
                                                                                                                                                                                                                                                                                                                                                                        34.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28778 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STAMEN AND CARPEL DEVELOPMENT IN WILD-TYPE
                                                                                                                                                                                                                                                                                                                                             46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROBABLE DIMERIZATION DOMAIN FOUND IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   THE MADS DOMAIN FAMILY OF TRANSCRIPTION
                                                                                                                                                                                                                                                                                                                                                                     Score 418.5; DB 1
Pred. No. 4.5e-21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  K-BOX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MADS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7C1EF7C96C19EACE CRC64
                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FACTOR INVOLVED IN REGULATING
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                                                                                                                                                                                                                                                                                                                                                                                                DB 1;
                                                                                                                                                                                                                                                                                                                                             63;
                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                Length
                                                                                                                                                                                                                                                                                                                                             47;
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                                                                                                                                                                                                                                                                                                                                       Gaps
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AGENTAL AGENTA
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                                           PROSITE; PS00350; MADS_BOX_1; 1.
PROSITE; PS50066; MADS_BOX_2; 1.
Transcription regulation; DNA-binding; Activator; Nuclear
                                                                                                                      Pfam; PF01486; K-box; 1.
Pfam; PF00319; SRF-TF; 1.
PRINTS; PR00404; MADSDOMAIN.
SMART; SM00432; MADS; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AG_PETHY
Q40885;
                                                                                                                                                                                                                         Mendel; 9809; PEThy; MADS; 8.
InterPro; IPR002487; K-box.
InterPro; IPR002100; MADS-box
                                                                                                                                                                                                                                                                                                          TRANSFAC;
                                                                                                                                                                                                                                                                                                                                                        EMBL; AB076051; BAB79434.1;
                                                                                                                                                                                                                                                                                                                                                                                     EMBL; X72912; CAA51417.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                   or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                   entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases -!- FUNCTION: PROBABLE TRANSCRIPTION FACTOR INVOLVED IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Petunia hybrida (Petunia).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15-DEC-1998 (Rel. 37, Last sequence up 01-MAR-2002 (Rel. 41, Last annotation
                             DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         petunia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Takatsuji H., Kapoor M., "Silencing of pMADS3 affects floral organ and meristem identity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-CV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Plant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tsuchimoto S., van der Krol A.R., Chua N.H., "Ectopic expression of pMADS3 in transgenic petunia phenocopies the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AGAMOUS protein (pMADS3).
                                                                                                                                                                                                                                                                                                                                     HSSP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     petunia blind mutant."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=94004017; PubMed=8104573;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=4102;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15-DEC-1998
15-DEC-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      _PETHY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FLOWERS (BY SIMILMANIA).
SUBCELLULAR LOCATION: Nuclear (By similarity).
TISSUE SPECIFICITY: EXPRESSED EXCLUSIVELY IN STAMENS AND CARPELS
TISSUE SPECIFICITY: MADS DOMAIN FAMILY OF TRANSCRIPTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIMILARITY: CONTAINS A PROBABLE DIMERIZATION DOMAIN FOUND IN SRF-TYPE TRANSCRIPTION FACTORS (K-BOX).
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                                                                                                                                                                                                                                                                                  ; P11746; Imm...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FUNCTION: PROBABLE TRANSCRIPTION FACTOR GENES THAT DETERMINES STAMEN AND CARPEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FACTORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SWISS-PROT entry is copyright. It is produced through een the Swiss Institute of Bioinformatics and the EM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mitchell;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5:843-853(1993).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 37, Created)
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K-BOX
                        MADS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              242 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         as its content
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Usage
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IN WILD-TYPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 a collaboration
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   commercial
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AGL5_ARATH STAN
P29385;
01-DEC-1992 (Rel. 2
01-DEC-1992 (Rel. 2
16-OCT-2001 (Rel. 4
              Pfam; PF01486; K-box; 1. Pfam; PF00319; SRF-TF; 1
                                                                                     EMBL; M55553; AAA327
PIR; E39534; E39534.
HSSP; P11746; 1MNM.
                                           TRANSFAC; T03028; -.
InterPro; IPR002487; K-box.
InterPro; IPR002100; MADS-box.
                                                                                                                                                  entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
                                                                                                                                                                              use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                homeotic and transcription factor genes.";
Genes Dev. 5:484-495(1991).
-!- FUNCTION: PROBABLE TRANSCRIPTION FACTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eueurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Arabidopsis thaliana (Mouse-ear cress).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  _ARATH
                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=91160981; PubMed=1672119;
                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Agamous-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           240 QL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           235 GL 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   181 QYLRAKIAETERSQQMNL-MPGSSSYDLVPPQQSFDARNYLQVNGLQTNNHYPRQDQPPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17
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                                                                                                                                                                                                                                                                                                                     SIMILARITY: BELONGS TO THE MADS DOMAIN FAMILY OF TRANSCRIPTION
                                                                                                                                                                                                                                                                         SRF-TYPE TRANSCRIPTION FACTORS (K-BOX).
                                                                                                                                                                                                                                                                                      SIMILARITY: CONTAINS A PROBABLE DIMERIZATION DOMAIN
                                                                                                                                                                                                                                                                                                                                       SUBCELLULAR LOCATION: Nuclear
                                                                                                                                                                                                                                                                                                             FACTORS
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                                                                                                                     M55553; AAA32735.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DELHKKIYETEGPSGVNRESPTPFNFAVV---ETRDVPVQLELSTLPQQNNIEPSTAPKL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SVKATIERYKKACSDSSNTGSIAEANAQ--YYQQEASKLRAQIGNLQNQNRNFLGESLAA 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SMKSVIDRYGKAKEEQQ----VVANPNSELKFWQREAASLRQQLHNLQENYRQLTGDDLSG 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LNLRDLRNLEQKIEKGISKIRAKKNELLFAEIEYMQKR-----EIDLHN-----NN
                                                                                                                                                                                                                                                                                                                                                                                             Yanofsky M.F., Meyerowitz E.M.; AGL6, an Arabidopsis gene family with similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            241
 PR00404;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 242 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MADS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Brassicales; Brassicaceae; Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
MADSDOMAIN
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24, Last seq
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27907 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  34.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No. 5e-;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 417.5;
Pred. No. 5e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A5249306B807A6BD CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    update)
                                                                                                                                                                                         There are no restrictions on ng as its content is in no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5e-21;
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RESULT AG_PANGI ID PANGI AG_PA AG Q408 DT 15-D DT 15-D DT 15-D DT 15-D DT 15-D DT 15-D ENAGE OC Eukas OC Sper OC Aste OX NCDJ RN [1] RP SEQUENC AG (In: CC -i-CC -
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Best Local
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use by non-profit institute. There are no restrictions on its modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AG_PANGI
Q40872;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids II; Apiales; Araliaceae; Panax.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS00350; MADS_BOX_1; 1.
PROSITE; PS50066; MADS_BOX_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SMART;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AGAMOUS protein (GAG2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (In) Plant Gene Register PGR95-060
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Panax ginseng (Korean ginseng)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kim Y.S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=4054;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "The cDNA sequence of two MADS box genes in Panax ginseng (GAG2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                242
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                                                                                                                                                                                                                                                                                                                                                                                         FUNCTION: PROBABLE TRANSCRIPTION FACTOR INVOLVED IN REGULATING GENES THAT DETERMINES STAMEN AND CARPEL DEVELOPMENT IN WILD-TYF FLOWERS (BY SIMILARITY).

SUBCELLULAR LOCATION: Nuclear (By similarity)
TISSUE SPECIFICITY: FLOWER. PREFERENTIALLY EXPRESSED IN STAMEN CARPEL AND WEAKLY IN PETAL. UNDETECTED IN LEAVES AND ROOTS.
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                                                                                                                                                                                                                                                                                                                                                                    CARPEL AND WEAKLY IN PETAL. UNDETECTED IN LEAVES SIMILARITY: BELONGS TO THE MADS DOMAIN FAMILY OF
                                                                                                                                                                                                                                                                                SRF-TYPE TRANSCRIPTION FACTORS (K-BOX).
                                                                                                                                                                                                                                                                                                            SIMILARITY: CONTAINS A
                                                                                                                                                                                SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lee H.S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18
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246 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       183
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hoon L.S., Yoo O.J., Chung W.I., Liu J.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            34.3%;
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                                                                                                                                                                                                                                                                                                            PROBABLE DIMERIZATION DOMAIN FOUND IN
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Pred. No. 5
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IN WILD-TYPE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR002487; K-box.
InterPro; IPR002100; MADS-box.
Pfam; PF01486; K-box; 1.
Pfam; PF00319; SRF-TF; 1.
                                                                                                                                                                                                                                                 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana.
                                                                                                                                                                                                                                                                                                                                        15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence up
16-OCT-2001 (Rel. 40, Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Transcription regulation; DNA-binding; Activator; Nuclear protein.
DOMAIN 19 73 MADS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS00350; MADS_BOX_1; PROSITE; PS50066; MADS_BOX_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRINTS; PR00404; MADSDOMAIN SMART; SM00432; MADS; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; Z46612; CAA86585.1;
HSSP; P11746; 1MNM
                                                                                   Kempin S.A., Mandel M.A., Yanofsky M.F.;

"Conversion of perianth into reproductive organs by ectopic expression of the tobacco floral homeotic gene NAG1.";

Plant Physiol. 103:1041-1046(193).

-!- FUNCTION: PROBABLE TRANSCRIPTION FACTOR INVOLVED IN REGULATING GENES THAT DETERMINES STAMEN AND CARPEL DEVELOPMENT IN WILD-TYPE
                                                                                                                                                                                                                                                                                                               AG1
                                                                                                                                                                                                                                                                                                                                                                                    Q43585;
                                                                                                                                                                                                                                                                                                                                                                                                  AG_TOBAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TRANSFAC; T03099;
                                                                                                                                                                                             STRAIN-CV
                                                                                                                                                                                                                                                                                            Nicotiana tabacum (Common tobacco).
                                                                                                                                                                                                                                     NCBI_TaxID=4097
                                                                                                                                                                                                                                                                                                                          AGAMOUS protein (NAG1).
                                         -!- SUBCELLULAR
                                                                                                                                                                            MEDLINE=94120000; PubMed=7507255
                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         238 ALQLV 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            175 QENDELHKKIYETEGPSGVNRESPTPFNFAVVETRDVPVQLELSTLPQQNNIEPSTAPKL 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     115 LSGLNVKELQSLENQLETSLRGVRAKKDHLLIDEIHDLNRKASLFHQENTDLYNKINLIR 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      235 GLQLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                188 AENERAQQHMNLMPGSSDYELAPPQSF------DGRNYIQLNGLQPNNHY--SRQDQT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    77
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MGRGKIVIRRIDNSTSRQVTFSKRRNGIFKKAKELAILCDAEVGLVIFSSTGRLYEYSST 60
                                                                                                                                                                                                                                                                                                                                                                                                                               9
 SIMILARITY:
SRF-TYPE TR!
                              FACTORS.
                                                          FLOWERS (BY SIMILARITY).
SUBCELLULAR LOCATION: Nuclear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SVKGTIERYKKACTD-----SPNTSSVSEANAQFYQQEASKLRQEISSIQKNNRNMMGES 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SMKSVIDRYGKAKEEQQVVANPN-----SELKFWQREAASLRQQLHNLQENYRQLTGDD 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LGSLTYRDLKGLETKLEKGISRIRSKKNELLFAEIEYMQKKEIDLHNNNQYLRAKI----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      95;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19
112
242 AA;
                                                                                                                                                                                          SAMSUN; TISSUE=Stamen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
 TRANSCRIPTION
                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                            BELONGS
                                                                                                                                                                                                                                                                                                                                                                   37, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              184
27781 MW;
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                                            TO
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FACTORS
                PROBABLE
                                            THE MADS DOMAIN FAMILY OF TRANSCRIPTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 414.5; DB Pred. No. 7.9e-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              K-BOX
                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0B3F02937B24CF76 CRC64;
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   (K-BOX)
                DIMERIZATION
                                                                                                                                                                                                                                                                                                                                                          update)
                                                                                                                                                                                                                                                                                                                                                                                                    248 AA.
                                                                                                                                                                                                                                                                                                                                         update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 242;
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AGENTAL AGENTA
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             _LYCES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AG_LYCES
Q40168;
15-DEC-1998
15-DEC-1998
16-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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SMART; SM00432; MADS; 1.
PROSITE; PS00350; MADS_BOX_1; 1.
PROSITE; PS50066; MADS_BOX_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF01486; K-box; 1. Pfam; PF00319; SRF-TF; 1
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InterPro; IPR002100; MADS-box.
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Pneuli L., Hareven D., Rounsley S.D., "Isolation of the tomato AGAMOUS gene homeotic role in transgenic plants.";
                                                                                                                          STRAIN=CV. VF36; TISSUE=Flower; MEDLINE=94198593; PubMed=7908549;
                                                                                                                                                                                                                                                                                                                                         Lycopersicon esculentum (Tomato).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eu
Asteridae; euasterids I; Solanales; Solanaceae; Solar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AG
                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AGAMOUS protein (TAG1).
                                                                                                                                                                                                                                                                                                 NCBI_TaxID=4081;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   237
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VKELQSLENQLETSLRGVRAKKDHLLIDEIHDLNRKASLFHQENTDLYNKINLIRQENDE 179
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               YTRQDQPSLQL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SVKATIERYKKACSDSSNTGSISEANAQYYQQEASKLRAQIGNLQNQNRNMLGESLAALS 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LRAKIAETERAQQQQQQQQMNLMPGSSSYELVPPPHQF---DTRN---YLQVNGLQTNNH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (Rel. 37, Created)
(Rel. 37, Last sequence update)
(Rel. 40, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                 Solanaceae; Solanum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     248 AA
                                           Yanofsky M.F., Lifschitz E.; TAG1 and analysis of its
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                                                                                                                                                                                                                                                                                                                                                                                         core eudicots;
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Best Local
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-i- FUNCTION: PROBABLE TRANSCRIPTION

GENES THAT DETERMINES STAMEN AND
FLOWERS (BY SIMILARITY).

-i- SUBCELLULAR LOCATION: Nuclear.

-i- SIMILARITY: BELONGS TO THE MADS D
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the European Bioinformatics Institute. There are no rest
use by non-profit institutions as long as its content
modified and this statement is not removed. Usage by ar
PRINTS; PR00404; MADSDOMAIN.
SMART; SM00432; MADS; 1.
PROSITE; PS00350; MADS BOX 1; 1.
PROSITE; PS50066; MADS_BOX_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF01486; K-box; 1
Pfam; PF00319; SRF-TF;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; L26295; AAA34197.1; -. HSSP; P11746; 1MNM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  entitles requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a
                                                                                                                                                                                                                                                          ARATH
AGL1_ARATH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Transcription regulation; DNA-binding; Activator; Nuclear protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR002487;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TRANSFAC; T03184;
                                                                                                                                                                                                                                                                                                                                                                                         235
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIMILARITY: CONTAINS A PROBABLE DIMERIZATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SRF-TYPE TRANSCRIPTION FACTORS (K-BOX).
                                                                                                                                                                                                                                                                                                                                                                                       NHYPRQDQPPIQL 247
                                                                                                                                                                                                                                                                                                                                                                                                                                         NNIEPSTAPKLGL 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QYLRAKIAETERAQHQHQQMNLMPGSSSNYHELVPPPQQF---DTRN---YLQVNGLQTN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MKLKELKNLEQRIEKGISKIRSKKNELLFAEIEYMQKR---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LNVKELQSLENQLETSLRGVRAKKDHLLIDEIHDLNRKASLFHQENTDLYNKINLIRQEN 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SVKATIERYKKACSDSSNTGSVSEANAQ--YYQQEASKLRAQIGNLMNQNRNMMGEALAG 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SMKSVIDRYGKAKEEQQ----VVANPNSELKFWQREAASLRQQLHNLQENYRQLTGDDLSG 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LGRGKIEIKRIENTINRQVIFCKRRNGLLKKAYELSVLCDAEVALVVFSNRGRLYEYANN 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DELHKKIYETE-----
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                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28723 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           49;
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9; Mismatches
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                                                                                                                                                                                                                                                               PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INVOLVED IN DEVELOPMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           69;
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IN WILD-TYP
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RA Reichelt J., Scharfe M., Schoen O., Bargues M., Teroll J., Climent J.,
RA Reichelt J., Scharfe M., Schoen O., Bargues M., Teroll J., Climent J.,
RA Cooke R., Laudie M., Berger-Llauro C., Purnelle B., Masuy D.,
RA Cooke R., Laudie M., Berger-Llauro C., Purnelle B., Masuy D.,
RA Mannan M., Maarse A.C., Alcaraz J.-P., Cottet A., Casacuberta E.,
RA Mannhaupt G., Haase D., Schoof H., Liguori R., Vitale D.,
RA Mannhaupt G., Haase D., Schoof H., Rudd S., Zaccaria P., Mewes H.-W.,
RA Mayer K.F.X., Kaul S., Town C.D., Koo H.L., Tallon L.J., Jenkins J.,
RA Rooney T., Rizzo M., Walts A., Utterback T., Fujli C.Y., Shea T.P.,
RA Rooney T., Rizzo M., Walts A., Utterback T., Fujli C.Y., Shea T.P.,
RA Rooney T., Rizzo M., Walts R., Wu D., Peterson J., Van Aken S.,
RA Rooney T., Rizzo M., Walts R., Wu D., Peterson J., Van Aken S.,
RA Preuss D., Lin X., Nierman W.C., Salzberg S.L., White O., Venter J.C.,
RA Preuss D., Kaneko T., Nakamura Y., Salzberg S.L., White O., Venter J.C.,
RA Fraser C.M., Kapeko T., Nakamura Y., Sato S., Kato T., Asamizu E.,
RA Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Murzaki A.,
RA Nakayama S., Nakazaki N., Shinpo S., Takeuchi C., Wada T.,
RA Watanabe A., Yamada M., Yasuda M., Tabata S.;

"Common P., Collied M., Tabata S.;
"Change C., Wanda M., Yasuda M., Tabata S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Desseny M., Boully M., Artiquenave F., Robert C., Brottier P. De Simone V., Choisne N., Artiquenave F., Robert C., Brottier F., Wincker P., Cattolico L., Weissenbach J., Saurin W., Quetier F., Schaefer M., Mueller-Auer S., Gabel C., Fuchs M., Benes V., Wurmbach E., Drzonek H., Erfle H., Jordan N., Bangert S., Winchenia R., Kranz H., Voss H., Holland R., Brandt P., Nyakatu Vezzi A., D'Angelo M., Pallavicini A., Toppo S., Simionati B., Conrad A., Hornischer K., Kauer G., Loehnert T.-H., Nordsiek G., Conrad A., Hornischer K., Kauer G., Loehnert T.-H., Toppo S., Simionati B., Conrad A., Hornischer K., Kauer G., Loehnert T.-H., Nordsiek G., Reichelt J., Scharfe M., Schoen O., Barques M., Terol J., Climen Reichelt J., Scharfe M., Schoen O., Barques M., Terol J., Climen
SEQUENCE
                                                                                                                                                                                         Pfam; PF01486; K-box; 1. Pfam; PF00319; SRF-TF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                          Transcription regulation; DNA-binding; Nuclear protein
                                                                                                                                                                             PRINTS;
                                                                                                                                                                                                                                                                                                                                                                                                                                         or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nature 408:820-822(2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Salanoubat M., Lemcke K., Rieger M., Ansorge W., Unseld M., Farthann B., Valle G., Bloecker H., Perez-Alonso M., Obermaier B., Delseny M., Boutry M., Grivell L.A., Mache R., Puigdomenech P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "AGLI-AGL6, an Arabidopsis gene family with similarity to floral homeotic and transcription factor genes."; Genes Dev. 5:484-495(1991).
                                                                                                                                                                                                                                                InterPro; IPR002100; MADS-box.
                                                                                                                                                                                                                                                                      InterPro; IPR002487; K-box
                                                                                                                                                                                                                                                                                               FRANSFAC; T03022;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Sequence and analysis of chromosome 3 of the plant Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=21016720; PubMed=11130713;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=91160981;    PubMed=1672119;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ween the Swiss Institute of Bioinfi
European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIMILARITY: BELONGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SRF-TYPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIMILARITY: CONTAINS A PROBABLE DIMERIZATION DOMAIN FOUND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FUNCTION: PROBABLE TRANSCRIPTION FACTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUBCELLULAR LOCATION: Nuclear
                                                                                                                                                                                                                                                                                                                                              A39534; A39534.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SWISS-PROT entry is copyright. It is produced through a collaboration en the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                             M55550; AAA32730.1;
                                                                                                                                                                                                                                                                                                                        P11746; 1MNM.
                                                                                                                                                                                                                                                                                                                                                                       AL353032;
                                                                                                                                                       SM00432; MADS; 1
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                                                                                                                                                                     PR00404; MADSDOMAIN.
                                                                                                     PS00350; MADS_BOX_1; 1. PS50066; MADS_BOX_2; 1.
         248 AA;
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                                                                                                                              MADS_BOX_1; 1.
            28336 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     institutions as long as its content
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TO THE MADS DOMAIN FAMILY OF
                                K-BOX
                                                           MADS
       D377C47F231F2099 CRC64
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15-DEC-1998
16-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                         Mandel M.A., Yanofsky M.F.;
"The Arabidopsis AGL8 MADS box gene is expressed in inflorescence meristems and is negatively regulated by APETALA1.";
Plant Cell 7:1763-1771(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embry,
Spermatophyta; Magnoliophyta; eudicotyledons;
                                                                                                                                                                                                                                                                                                  "Structural analysis of Arabidopsis thaliana chromosome Sequence features of the regions of 1,191,918 bp covered
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15-DEC-1998 (Rel. 37, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation updat
Agamous-like MADS box protein AGL8.
AGL8 OR AT5660910 OR MSL3.3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ARATH
                                                                                                                                                                                                                                                                                     physically assigned P1 clones.";
                                                                                                                                                                                                                                                                                                                                     Tabata S.;
                                                                                                                                                                                                                                                                                                                                                 Nakamura Y., Sato S., Kaneko
                                                                                                                                                                                                                                                                                                                                                                MEDLINE=98162728;
                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=96093419; PubMed=8535133;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q38876;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            193 NPDQQESSVIQGTTVYE----SGVS
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                                                                                                                                                                                            SUBCELLULAR LOCATION: Nuclear (By similarity).
DEVELOPMENTAL STAGE: DRAMATICALLY UP-REGULATED UPON THE TRANSITION
FROM VEGETATIVE TO REPRODUCTIVE DEVELOPMENT, WHERE ITS EXPRESSION
IS DETECTED IN CAULINE LEAVES, STEMS, AND IN FLOWERS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MGRGKIVIRRIDNSTSRQVTFSKRRNGIFKKAKELAILCDAEVGLVIFSSTGRLYEYSST 60
                                                                                                                                                                                                                                                       Res. 4:401-414(1997).
FUNCTION: PROBABLE TRANSCRIPTION FACTOR.
                                                                                                                                                                                SIMILARITY: BELONGS TO THE MADS DOMAIN FAMILY OF
                                                                                                                                  SRF-TYPE TRANSCRIPTION FACTORS
                                                                                                                                                SIMILARITY: CONTAINS A PROBABLE DIMERIZATION DOMAIN FOUND
                                                                                  SWISS-PROT entry is copyright. It is produced through a ceen the Swiss Institute of Bioinformatics and the EMBL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SMKSVIDRYGKAKEEQQVVANPNS----ELKFWQREAASLRQQLHNLQENYRQLTGDDLS 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LGRGKIEIKRIENTINRQVTFCKRRNGLLKKAYELSVLCDAEVALVIFSTRGRLYEYANN
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                                                                                                                                                                                                                                                                                                                                                                PubMed=9501997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  37, Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Brassicaceae; Arabidopsis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                Kotani H., Asamizu E.,
                                                                                                                                   (K-BOX)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3.4e-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Embryophyta; Tracheophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A
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                                                                                       a collaboration
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AGL8_SINAL
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Best Local S
Matches 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q41274;
15-DEC-1998 (Rel. 3
15-DEC-1998 (Rel. 3
16-OCT-2001 (Rel. 4
This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN
                                                                                                                                                                                           -1- FUNCTION: PROBABLE TRANSCRIPTION FACTOR
-1- SUBCELLULAR LOCATION: Nuclear (By simila-
-1- DEVELOPMENTAL STAGE: EXPRESSED IN APICAL
                                                                                                                                                                                                                                                                                                              Menzel G., Apel K., Melzer S.; "Identification of two MADS box genes that are expressed in the apical meristem of the long-day plant Sinapis alba in transition
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosid eurosids II; Brassicales; Brassicaceae; Sinapis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro;
Pfam; PF01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sinapis alba (White mustard) (Brassica hirta).
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                                                                                                                                                                                                                                                                                 Plant
                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=97077349; PubMed=8919916;
                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE=Flower;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Agamous-like MADS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AGL8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=3728;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
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DOMAIN 3 57 MADS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS00350; MADS_BOX_1; PROSITE; PS50066; MADS_BOX_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRINTS; PR00404; MADSDOMAIN. SMART; SM00432; MADS; 1.
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TRANSFAC; T03030; -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            174
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                                                                   SIMILARITY: CONTAINS A PROBABLE DIMERIZATION DOMAIN FOUND SRF-TYPE TRANSCRIPTION FACTORS (K-Box).
                                                                                                                                               SIMILARITY: BELONGS TO THE MADS DOMAIN FAMILY OF TRANSCRIPTION
                                                                                                                                                                                 TO FLOWERING.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            S-MKSVIDRYGK-AKEEQQVVANPNSELKFWQREAASLRQQLHNLQENYRQLTGDDLSGL 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MGRGRVQLKRIENKINRQVTFSKRRSGLLKKAHEISVLCDAEVALIVFSSKGKLFEYSTD 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EREKKTGQQEGQLVQCSNSSSVLLPQYCVTSSRDGFVERVGGENGGASSLTEPNSLLPA 232
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                                                                                                                                                                                                                                                                            9:399-408(1996)
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IPR002100; MADS-box.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   242 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BAB10640.1; -
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37,
40,
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        55;
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                                                                                                                                                                                           (By similarity).
) IN APICAL MERISTEMS IN TRANSITION
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EMBL
  a collaboration
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Q40170;
15-DEC-1998
15-DEC-1998
16-OCT-2001
                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN-CV. VFNT CHERRY; TISSUE-Flower;
                                                 -!- FUNCTION: PROBABLE TRANSCRIPTION FACTOR.
-!- SUBCELLULAR LOCATION: Nuclear (By similarity).
-!- TISSUE SPECIFICITY: FLOWER-SPECIFIC.
                                                                                                                                homeotic genes from Antirrhinum and Arabidopsis."; Plant J. 1:255-266(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LYCES
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Viridiplantae; Streptophyta; Embry Spermatophyta; Magnoliophyta; eudicotyledons;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lycopersicon esculentum (Tomato).
Eukaryota; Viridiplantae; Strepto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TDR4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                       floral development,
                                                                                                                                                                                                              "The MADS box gene family in tomato: temporal expression
                                                                                                                                                                                                                                                                      Pnueli L., Abu-Abeid M., Zamir D., Nacken W.,
                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=4081;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Agamous-like MADS box protein AGL8 homolog (TM4)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Transcription regulation; DNA-binding; Nuclear protein DOMAIN 3 57 MADS. DOMAIN 97 169 K-BOX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS00350; MADS_BOX_1; 1. PROSITE; PS50066; MADS_BOX_2; 1.
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InterPro; IPR002487; K-box.
InterPro; IPR002100; MADS-box.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; U25695; AAB41525.1; -. HSSP; P11746; 1MNM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                 Lifschitz E.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 179
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                       SIMILARITY: BELONGS TO THE MADS DOMAIN FAMILY OF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 169 P
; 27660 MW;
                                                                                                                                                                                    conserved secondary structures and homology with
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36.3%;
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                                                                                                                                                                                                                                                                   Schwarz-Sommer Z.,
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                       TRANSCRIPTION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           09FUY6;
01-MAR-2002 (Rel. 41, Created)
01-MAR-2002 (Rel. 41, Last seq
01-MAR-2002 (Rel. 41, Last anno
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PROSITE; PS50066; MADS_BOX_2; 1.
Transcription regulation; DNA-binding; Nuclear protein.
DOMAIN 3 57
MADS.
DOMAIN 97 169
K-BOX.
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                                                                                                                          STRAIN-cv. Heinz 1706;
MEDLINB-20426111; PubMed=10972295;
Mao L., Begum D., Chuang H.W., Budiman M.A., Szymkowiak E.J.,
Irish E.E., Wing R.A.;
"JOINTLESS is a MADS-box gene controlling tomato flower abscission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF01486; K-box; 1. Pfam; PF00319; SRF-TF; 1
                                          zone development.";
Nature 406:910-913(2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Asteridae; euasterids I;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
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                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=4081;
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                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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FUNCTION: PUTATIVE TRANSCRIPTION FACTOR THAT COORDINATES GENE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QLSKKVKEREKSAQQISGINSSSLFAHTDFYLGTYQSTNV 206
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MGRGRVQLKRIENKINRQVTFSKRRSGLLKKAHEISVLCDAEVGLIVFSTKGKLFEYAND
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SM00432; MADS; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         227 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26403 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     institutions as long
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Solanales; Solanaceae; Solanum
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (LeMADS)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                annotation
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Pred. No. 5.1e-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4976195B3BDE53F5
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MBL outstation -
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRINTS; PR00404; MADSDOMAIN.
SMART; SM00432; MADS; 1.
PROSITE; PS00350; MADS; BOX_1; 1.
PROSITE; PS50066; MADS_BOX_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF01486; K-box; 1 Pfam; PF00319; SRF-TF;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AF275345; AAG09811.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nuclear protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Transcription regulation; DNA-binding; Developmental protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR002487; K-box.
InterPro; IPR002100; MADS-box.
                                                                    177
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                                   221
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                                                                                                                                                                                                                                       61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                fruits which are widely used in the processing tomato industry the fruits support mechanical harvesting and are not subject to physical wounding during transportation.

SIMILARITY: BELONGS TO THE MADS DOMAIN FAMILY OF TRANSCRIPTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUBCELLULAR LOCATION: Nuclear (Probable).
TISSUE SPECIFICITY: WIDELY EXPRESSED WITH HIGHEST LEVELS IN SHOOT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIMILARITY: CONTAINS 1 PROBABLE DIMERIZATION DOMAIN FOUND IN SRF-
TYPE TRANSCRIPTION FACTORS (K-BOX).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BIOTECHNOLOGY: Mutation in 'JOINTLESS' yields 'stemless' tomato
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EXPRESSION UNDERLYING THE DIFFERENTIATION OF THE PEDICEL ABSCISSION ZONE. MAY ALSO BE INVOLVED IN THE MAINTENANCE OF THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TIPS AND AXILLARY BUDS. ALSO FOUND IN FULLY DEVELOPED PEDICELS AND
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                                                                                                                                                                                                                                                                                                  MGRGKIVIRRIDNSTSRQVTFSKRRNGIFKKAKELAILCDAEVGLVIFSSTGRLYEYSST 60
                                                                                                                                                                     SGLNVKELQSLENQLETSLRGVRAKKDHLLIDEIHDLNRKASLFHQENTDLYNKINLIRQ 175
                                                                                                                                                                                                                                                                     MAREKIQIKKIDNSTARQVTFSKRRRGLFKKAEELSVLCDADVALIIFSSTGKLFDYSSS 60
PPODDDSSDTSLKLGL
                                 POQUNIEPSTAPKLGL
                                                                   NNNNNNGYREAGYVIFEPENGFNNNNNEDGQSSESVTNPCNSI-
                                                                                                    END-----ELHKKIYETE------GPSGVNRESPT-PENFAVVETRDVPVQLELSTL
                                                                                                                                      QGLNIEELQQLERSLETGLSRVIERKGDKIMREINQLQQKGMHLMEENEKLRQQVMEISN 176
                                                                                                                                                                                                     SMKQILERRDLHSKNLEKLDQPSLELQLVENSNYSRLSKEISEKSHRL----RQMRGEEL 116
                                                                                                                                                                                                                                     SMKSVIDRYGKAKEEQQVVANPNSELKF-----WQREAASLRQQLHNLQENYRQLTGDDL 115
                                                                                                                                                                                                                                                                                                                                                         Similarity
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                                                                                                                                                                                                                                                                                                                                         Conservative
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Pred. No. 6.6e-19;
                                                                                                                                                                                                                                                                                                                                                                                                                                          POLY-ASN.
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                                                                                                                                                                                                                                                                                                                                                                         Length 265;
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Search completed: Job time: 502 sec

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